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(FILE 'HOME' ENTERED AT 14:32:50 ON 11 AUG 2006)

FILE 'MEDLINE, AGRICOLA, BIOSIS, CAPLUS, EMBASE, SCISEARCH' ENTERED AT
14:33:09 ON 11 AUG 2006

 E KERSCHBAUMER R/AU
L1 64 E3 OR E5 OR E6 OR E4
 E SCHEIFLINGER F/AU
L2 233 E3 OR E5
L3 273 L1 OR L2
L4 22760 (FACTOR (W) (IX OR IXA OR NINE)) OR FIXA OR F-IX OR F-IXA OR FAC
L5 3410026 ANTIBODY OR ANTIBODIES OR IMMUNOGLOBULIN OR IMMUNOGLOBULINS OR
L6 17 L3 AND L4
L7 9 DUP REM L6 (8 DUPLICATES REMOVED)
L8 3200 L4 (P) L5
L9 1855 L4 (S) L5
L10 510445 PROCOAGULANT OR COAGULANT OR COAGULATION OR CLOT OR CLOTTING
L11 386078 THROMBUS OR THROMBI OR THROMBOSIS
L12 941 L9 (P) (L10 OR L11)
L13 481 L9 (S) (L10 OR L11)
L14 0 224F3
L15 0 198B1
L16 0 224/F3 OR 198/B1
L17 0 (224(W)F3) OR (198(W)B1)
L18 0 (224-F3) OR (198-B1)
L19 104138 (FACTOR(W) (X OR XA OR VIII OR VIIIA)) OR FXA OR FVIII OR FVIII
L20 370 L12(P)L19
L21 140 L13(P)L19
L22 65 DUP REM L21 (75 DUPLICATES REMOVED)

=>

EAST Search History

Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L1	10	((("4395396") or ("4873316") or ("5932706") or ("6632927") or ("6391299")).PN.	US-PGPUB; USPAT; USOCR; EPO; JPO; DERWENT	OR	OFF	2006/08/11 14:25
L2	0	("(factoradj(IXorIXa))orF-IXorF-IXaorfIXa").PN.	US-PGPUB; USPAT; USOCR; EPO; JPO; DERWENT	OR	OFF	2006/08/11 14:27
L3	356	(factor adj (IXorIXa)) or F-IX or F-IXa or fIXa	US-PGPUB; USPAT; EPO; JPO; DERWENT	ADJ	ON	2006/08/11 14:28
L4	302951	antibody or antibodies or immunoglobulin or immunoglobulins or IgG or IgE or IgA or IgM or Fab or Fv or scFv or sFv or Fab'	US-PGPUB; USPAT; EPO; JPO; DERWENT	ADJ	ON	2006/08/11 14:29
L5	31	I3 with I4	US-PGPUB; USPAT; EPO; JPO; DERWENT	ADJ	ON	2006/08/11 14:29
L6	83	I3 same I4	US-PGPUB; USPAT; EPO; JPO; DERWENT	ADJ	ON	2006/08/11 14:30
L7	106	kerschbaumer.in.	US-PGPUB; USPAT; EPO; JPO; DERWENT	ADJ	ON	2006/08/11 14:30
L8	42	scheiflinger.in.	US-PGPUB; USPAT; EPO; JPO; DERWENT	ADJ	ON	2006/08/11 14:31
L9	5	(I7 or I8) and I3	US-PGPUB; USPAT; EPO; JPO; DERWENT	ADJ	ON	2006/08/11 14:40
L10	7	224F3 or 198B1	US-PGPUB; USPAT; EPO; JPO; DERWENT	ADJ	ON	2006/08/11 14:42
L11	3	224/F3 or 198/B1	US-PGPUB; USPAT; EPO; JPO; DERWENT	ADJ	ON	2006/08/11 14:48

EAST Search History

L12	41	("224" adj F3) or ("198" adj B1)	US-PGPUB; USPAT; EPO; JPO; DERWENT	ADJ	ON	2006/08/11 14:48
L13	3	l12 same l4	US-PGPUB; USPAT; EPO; JPO; DERWENT	ADJ	ON	2006/08/11 14:48

Result No.	Score	% Query Match	Length	DB	ID	Description
1	663	100.0	125	9	ADY75166	Ady75166 Antibody
2	570	86.0	119	6	ABJ18572	Abj18572 Ganglioside
3	570	86.0	119	6	ABJ18570	Abj18570 Ganglioside
4	569	85.8	555	4	AAB19871	Aab19871 Activatin
5	569	85.8	565	4	AAB19873	Aab19873 Activatin
6	569	85.8	577	4	AAB19872	Aab19872 Activatin
7	569	85.8	704	4	AAB19888	Aab19888 MLV envel
8	527.5	79.6	118	8	ADP79643	Adp79643 8H9 VH. 1
9	523.5	79.0	243	7	ABM78998	Abm78998 Monoclonal
10	523.5	79.0	243	8	ADP79638	Adp79638 8H9 scFv.
11	522.5	78.8	116	2	AAR79241	Aar79241 Heavy chain
12	519.5	78.4	243	7	ABM78999	Abm78999 Monoclonal
13	519.5	78.4	243	8	ADP79639	Adp79639 8H9 scFv
14	516.5	77.9	139	6	ABG74245	Abg74245 Mouse anti
15	509	76.8	246	9	ADW64805	Adw64805 Murine si
16	509	76.8	246	9	ADW64803	Adw64803 Murine si
17	508	76.6	138	8	ADI26639	Adi26639 Mouse anti
18	506	76.3	259	9	AEA29819	Aea29819 Mouse high
19	505.5	76.2	139	2	AAW29750	Aaw29750 Anti-HMFG
20	505	76.2	119	6	AAE33325	Aae33325 12E anti
21	505	76.2	119	9	ADZ21523	Adz21523 Anti-Muc-
22	505	76.2	243	9	AED66562	Aed66562 Anti-coll
23	505	76.2	281	6	AAE33333	Aae33333 12E anti
24	505	76.2	281	9	ADZ21537	Adz21537 Anti-Muc-
25	504.5	76.1	120	8	ADH17838	Adh17838 Murine an
26	504.5	76.1	120	9	ADW11469	Adw11469 Murine an
27	504.5	76.1	120	9	ADW86139	Adw86139 Novel cyt
28	504.5	76.1	120	9	AEC05642	Aec05642 lae6 anti
29	504.5	76.1	120	9	AED65315	Aed65315 Heavy chain
30	503.5	75.9	119	8	ADO32159	Ado32159 Mouse anti
31	503.5	75.9	138	3	AAV56873	Aay56873 MAb CT-M-
32	502	75.7	119	8	ADN36310	Adn36310 Rat anti-
33	502	75.7	261	8	ADN36312	Adn36312 Rat anti-
34	501	75.6	119	6	AAE33327	Aae33327 3D antibo
35	501	75.6	119	9	ADZ21525	Adz21525 Anti-Muc-
36	501	75.6	194	6	AAE33334	Aae33334 3D antibo
37	501	75.6	194	9	ADZ21538	Adz21538 Anti-Muc-
38	498.5	75.2	139	2	AAR33950	Aar33950 CTMO1 VH.
39	498	75.1	241	10	AEF25222	Aef25222 Mouse anti
40	497	75.0	118	8	ADN62634	Adn62634 HIV gp 41
41	496	74.8	119	10	AEF12980	Aef12980 Mouse E34
42	492	74.2	117	8	ADH17836	Adh17836 Murine an
43	492	74.2	117	9	ADW11467	Adw11467 Murine an
44	492	74.2	117	9	ADW86134	Adw86134 Novel cyt
45	492	74.2	117	9	AEC05640	Aec05640 lplg anti
46	492	74.2	117	9	AED65313	Aed65313 Heavy chain
47	492	74.2	123	3	AAV78325	Aay78325 Anti-zeta
48	492	74.2	532	3	AAV78328	Aay78328 Bispecific
49	490.5	74.0	118	3	AAB11391	Aab11391 Murine II
50	490.5	74.0	269	8	ADR28054	Adr28054 NPB polyp
51	490	73.9	118	7	ADP43262	Adp43262 Antibody
52	489.5	73.8	127	9	ADY22015	Ady22015 Antibody
53	489.5	73.8	271	5	ABG31022	Abg31022 Mouse sin
54	489.5	73.8	271	7	ADD25451	Add25451 Binding d
55	489.5	73.8	271	7	ADM42726	Adm42726 Synthetic
56	489.5	73.8	271	9	AEB95394	Aeb95394 Mouse HD3
57	489.5	73.8	271	9	AEB94428	Aeb94428 Mouse anti

SCORE Search Results Details for Application 10661366 and Search Result us-10-661-366-1.

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This page gives you Search Results detail for the Application 10661366 and Search Result us-10-661-366-1.

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OM protein - protein search, using sw model

Run on: August 9, 2006, 08:17:00 ; Search time 82.3379 Seconds
(without alignments)
132.883 Million cell updates/sec

Title: US-10-661-366-1
Perfect score: 663
Sequence: 1 QVQMQQSGAELVKPGASVKL.....GSYYYAMDYWGQGTSTVTVSS 125

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Issued_Patents_AA:*
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3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	522.5	78.8	116	1	US-08-888-366-2	Sequence 2, Appli
2	504.5	76.1	139	1	US-08-253-877C-8	Sequence 8, Appli

3	504.5	76.1	139	1	US-08-452-164A-8	Sequence 8, Appli
4	503.5	75.9	138	2	US-08-603-024-2	Sequence 2, Appli
5	486	73.3	119	2	US-09-556-605-1	Sequence 1, Appli
6	486	73.3	219	2	US-09-254-180C-131	Sequence 131, App
7	486	73.3	219	2	US-09-254-180C-181	Sequence 181, App
8	484	73.0	291	3	US-09-661-992B-102	Sequence 102, App
9	484	73.0	322	3	US-09-661-992B-96	Sequence 96, Appl
10	484	73.0	729	3	US-09-661-992B-94	Sequence 94, Appl
11	481.5	72.6	120	1	US-08-211-202-1	Sequence 1, Appli
12	481.5	72.6	246	1	US-08-469-486-57	Sequence 57, Appl
13	481.5	72.6	246	1	US-08-469-658-57	Sequence 57, Appl
14	479.5	72.3	118	2	US-08-766-350B-48	Sequence 48, Appl
15	479	72.2	247	2	US-10-620-049-21	Sequence 21, Appl
16	476.5	71.9	128	1	US-08-202-047-21	Sequence 21, Appl
17	476.5	71.9	128	2	US-08-964-690-21	Sequence 21, Appl
18	475.5	71.7	249	1	US-08-797-689-18	Sequence 18, Appl
19	475.5	71.7	249	2	US-09-984-186-18	Sequence 18, Appl
20	475.5	71.7	249	2	US-10-237-866-18	Sequence 18, Appl
21	475.5	71.7	249	2	US-10-702-636-18	Sequence 18, Appl
22	475.5	71.7	249	2	US-10-702-536-18	Sequence 18, Appl
23	473	71.3	117	2	US-09-157-370-2	Sequence 2, Appli
24	471.5	71.1	139	1	US-08-137-117D-35	Sequence 35, Appl
25	471.5	71.1	139	1	US-08-436-717-35	Sequence 35, Appl
26	471.5	71.1	273	1	US-08-403-853-18	Sequence 18, Appl
27	470	70.9	119	2	US-08-767-128-6	Sequence 6, Appli
28	469.5	70.8	140	2	US-09-724-138-44	Sequence 44, Appl
29	469.5	70.8	140	2	US-09-630-198-44	Sequence 44, Appl
30	469	70.7	119	1	US-08-553-497A-12	Sequence 12, Appl
31	468.5	70.7	120	2	US-08-397-411-11	Sequence 11, Appl
32	468.5	70.7	139	1	US-08-656-586-4	Sequence 4, Appli
33	468.5	70.7	269	1	US-08-428-257A-72	Sequence 72, Appl
34	468.5	70.7	269	1	US-08-491-988-3	Sequence 3, Appli
35	468.5	70.7	402	1	US-08-491-988-9	Sequence 9, Appli
36	468.5	70.7	415	1	US-08-491-988-7	Sequence 7, Appli
37	468.5	70.7	435	1	US-08-491-988-5	Sequence 5, Appli
38	468	70.6	121	2	US-08-913-555-19	Sequence 19, Appl
39	467.5	70.5	122	2	US-08-767-128-4	Sequence 4, Appli
40	467	70.4	121	2	US-08-881-037-65	Sequence 65, Appl
41	467	70.4	140	2	US-08-475-815B-11	Sequence 11, Appl
42	467	70.4	470	2	US-09-238-741-4	Sequence 4, Appli
43	466.5	70.4	116	2	US-09-244-592-1	Sequence 1, Appli
44	466.5	70.4	120	2	US-10-092-246-12	Sequence 12, Appl
45	466.5	70.4	120	2	US-10-096-246A-12	Sequence 12, Appl
46	466.5	70.4	244	2	US-09-244-369B-1	Sequence 1, Appli
47	466.5	70.4	244	2	US-09-940-391-1	Sequence 1, Appli
48	466	70.3	120	2	US-09-065-059-1	Sequence 1, Appli
49	466	70.3	120	2	US-08-913-555-1	Sequence 1, Appli
50	466	70.3	121	2	US-09-232-290-59	Sequence 59, Appl
51	466	70.3	244	1	US-08-553-497A-22	Sequence 22, Appl
52	465.5	70.2	120	2	US-10-351-748-24	Sequence 24, Appl
53	465.5	70.2	122	2	US-10-092-246-10	Sequence 10, Appl
54	465.5	70.2	122	2	US-10-092-246-11	Sequence 11, Appl
55	465.5	70.2	122	2	US-10-096-246A-10	Sequence 10, Appl
56	465.5	70.2	122	2	US-10-096-246A-11	Sequence 11, Appl
57	465	70.1	445	1	US-08-353-400-33	Sequence 33, Appl
58	465	70.1	464	1	US-08-353-400-36	Sequence 36, Appl
59	464	70.0	244	1	US-08-553-497A-20	Sequence 20, Appl
60	464	70.0	246	1	US-08-553-497A-24	Sequence 24, Appl
61	464	70.0	247	2	US-10-620-049-23	Sequence 23, Appl
62	464	70.0	247	2	US-10-620-049-25	Sequence 25, Appl
63	463	69.8	119	2	US-08-881-037-62	Sequence 62, Appl

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OM protein - protein search, using sw model

Run on: August 9, 2006, 09:01:05 ; Search time 267.491 Seconds
(without alignments)
216.462 Million cell updates/sec

Title: US-10-661-366-1
Perfect score: 663
Sequence: 1 QVQMQQSGAELVKPGASVKL.....GSYYYAMDYWGQGTSTVTVSS 125

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Published_Applications_AA_Main:*
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2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	663	100.0	125	5 US-10-661-366-1	Sequence 1, Appli
2	570	86.0	119	5 US-10-473-977-67	Sequence 67, Appl
3	527.5	79.6	118	5 US-10-537-061-7	Sequence 7, Appli

4	523.5	79.0	243	4	US-10-097-558-2	Sequence 2, Appli
5	523.5	79.0	243	5	US-10-505-658-2	Sequence 2, Appli
6	523.5	79.0	243	5	US-10-537-061-2	Sequence 2, Appli
7	519.5	78.4	243	4	US-10-097-558-3	Sequence 3, Appli
8	519.5	78.4	243	5	US-10-505-658-3	Sequence 3, Appli
9	519.5	78.4	243	5	US-10-537-061-3	Sequence 3, Appli
10	516.5	77.9	139	4	US-10-006-773-13	Sequence 13, Appl
11	509	76.8	246	5	US-10-861-617-15	Sequence 15, Appl
12	509	76.8	246	5	US-10-861-617-17	Sequence 17, Appl
13	508	76.6	138	2	US-08-779-784-31	Sequence 31, Appl
14	508	76.6	138	4	US-10-010-729-67	Sequence 67, Appl
15	505	76.2	119	4	US-10-112-788-1	Sequence 1, Appli
16	505	76.2	119	4	US-10-435-614-1	Sequence 1, Appli
17	505	76.2	281	4	US-10-112-788-9	Sequence 9, Appli
18	505	76.2	281	4	US-10-435-614-15	Sequence 15, Appl
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20	504.5	76.1	120	5	US-10-895-135-59	Sequence 59, Appl
21	504.5	76.1	120	5	US-10-897-406-78	Sequence 78, Appl
22	504.5	76.1	120	5	US-10-932-334-78	Sequence 78, Appl
23	503.5	75.9	119	5	US-10-700-632-75	Sequence 75, Appl
24	502	75.7	119	4	US-10-689-921-5	Sequence 5, Appli
25	502	75.7	261	4	US-10-689-921-7	Sequence 7, Appli
26	501	75.6	119	4	US-10-112-788-3	Sequence 3, Appli
27	501	75.6	119	4	US-10-435-614-3	Sequence 3, Appli
28	501	75.6	194	4	US-10-112-788-10	Sequence 10, Appl
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30	498	75.1	241	5	US-10-902-546-6	Sequence 6, Appli
31	496	74.8	119	6	US-11-226-886-46	Sequence 46, Appl
32	496	74.8	119	6	US-11-159-046-12	Sequence 12, Appl
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34	492	74.2	117	5	US-10-895-135-54	Sequence 54, Appl
35	492	74.2	117	5	US-10-897-406-76	Sequence 76, Appl
36	492	74.2	117	5	US-10-932-334-76	Sequence 76, Appl
37	492	74.2	123	6	US-11-036-098-14	Sequence 14, Appl
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55	488	73.6	116	5	US-10-700-632-74	Sequence 74, Appl
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57	486	73.3	119	3	US-09-839-447A-1	Sequence 1, Appli
58	486	73.3	119	4	US-10-153-271-1	Sequence 1, Appli
59	486	73.3	119	4	US-10-369-060A-1	Sequence 1, Appli
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61	486	73.3	119	6	US-11-188-187A-1	Sequence 1, Appli
62	485	73.2	290	6	US-11-032-773-957	Sequence 957, App
63	485	73.2	319	6	US-11-032-773-955	Sequence 955, App
64	484	73.0	291	6	US-11-093-103-102	Sequence 102, App

SCORE Search Results Details for Application 10661366 and Search Result us-10-661-366-1.rapbn.

Score Home	Retrieve Application	SCORE System	SCORE	Comments /
Page	List	Overview	FAQ	Suggestions

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OM protein - protein search, using sw model

Run on: August 9, 2006, 09:02:15 ; Search time 40.9556 Seconds
(without alignments)
205.442 Million cell updates/sec

Title: US-10-661-366-1
Perfect score: 663
Sequence: 1 QVQMQQSGAELVKPGASVKL.....GSYYYAMDYWGQGTSTVTVSS 125

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 239914 seqs, 67312017 residues

Total number of hits satisfying chosen parameters: 239914

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Published_Applications_AA_New:*
1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
8: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	% Query
--------	------------

No.	Score	Match	Length	DB	ID	Description
1	508	76.6	138	7	US-11-224-664-31	Sequence 31, Appl
2	504.5	76.1	120	7	US-11-290-687-70	Sequence 70, Appl
3	492	74.2	117	7	US-11-290-687-68	Sequence 68, Appl
4	490.5	74.0	269	6	US-10-539-402-1	Sequence 1, Appli
5	479	72.2	247	7	US-11-270-894-1	Sequence 1, Appli
6	475.5	71.7	249	7	US-11-330-353-18	Sequence 18, Appl
7	473.5	71.4	120	7	US-11-290-687-67	Sequence 67, Appl
8	473.5	71.4	122	7	US-11-254-182-28	Sequence 28, Appl
9	473.5	71.4	122	7	US-11-106-762-11	Sequence 11, Appl
10	473.5	71.4	122	7	US-11-238-281-7	Sequence 7, Appli
11	473.5	71.4	122	7	US-11-291-698A-47	Sequence 47, Appl
12	472.5	71.3	120	7	US-11-290-687-61	Sequence 61, Appl
13	472	71.2	118	6	US-10-684-237-12	Sequence 12, Appl
14	467	70.4	121	7	US-11-256-060-2	Sequence 2, Appli
15	467	70.4	140	7	US-11-183-218-62	Sequence 62, Appl
16	467	70.4	451	6	US-10-822-231-4	Sequence 4, Appli
17	467	70.4	451	6	US-10-822-231-5	Sequence 5, Appli
18	467	70.4	451	7	US-11-174-287-5	Sequence 5, Appli
19	467	70.4	451	7	US-11-174-287-7	Sequence 7, Appli
20	467	70.4	451	7	US-11-256-060-17	Sequence 17, Appl
21	465.5	70.2	120	7	US-11-290-687-63	Sequence 63, Appl
22	462.5	69.8	120	7	US-11-290-687-72	Sequence 72, Appl
23	460	69.4	235	7	US-11-155-909-24	Sequence 24, Appl
24	460	69.4	255	7	US-11-155-909-21	Sequence 21, Appl
25	460	69.4	297	7	US-11-155-909-19	Sequence 19, Appl
26	459	69.2	125	7	US-11-219-563-79	Sequence 79, Appl
27	452.5	68.3	122	7	US-11-224-664-28	Sequence 28, Appl
28	452.5	68.3	242	7	US-11-183-325-20	Sequence 20, Appl
29	452	68.2	125	7	US-11-006-808-44	Sequence 44, Appl
30	451.5	68.1	120	7	US-11-290-687-62	Sequence 62, Appl
31	450.5	67.9	118	7	US-11-290-687-59	Sequence 59, Appl
32	448	67.6	115	6	US-10-570-220-82	Sequence 82, Appl
33	447.5	67.5	242	7	US-11-183-325-18	Sequence 18, Appl
34	444.5	67.0	132	6	US-10-513-539A-2	Sequence 2, Appli
35	442.5	66.7	124	7	US-11-290-687-65	Sequence 65, Appl
36	442.5	66.7	124	7	US-11-290-687-69	Sequence 69, Appl
37	442	66.7	119	7	US-11-183-218-54	Sequence 54, Appl
38	442	66.7	143	7	US-11-224-664-26	Sequence 26, Appl
39	441	66.5	121	7	US-11-061-841-20	Sequence 20, Appl
40	441	66.5	123	7	US-11-006-808-9	Sequence 9, Appli
41	439.5	66.3	124	7	US-11-290-687-66	Sequence 66, Appl
42	438.5	66.1	121	6	US-10-522-086-2	Sequence 2, Appli
43	438.5	66.1	123	7	US-11-290-687-60	Sequence 60, Appl
44	438.5	66.1	167	7	US-11-301-373-56	Sequence 56, Appl
45	437.5	66.0	119	6	US-10-968-757-17	Sequence 17, Appl
46	436.5	65.8	132	6	US-10-513-539A-6	Sequence 6, Appli
47	436	65.8	117	6	US-10-684-237-14	Sequence 14, Appl
48	435.5	65.7	123	7	US-11-290-687-58	Sequence 58, Appl
49	435.5	65.7	123	7	US-11-290-687-64	Sequence 64, Appl
50	434.5	65.5	118	7	US-11-297-317-2	Sequence 2, Appli
51	434.5	65.5	448	7	US-11-297-317-4	Sequence 4, Appli
52	433.5	65.4	139	6	US-10-533-104A-21	Sequence 21, Appl
53	433.5	65.4	139	6	US-10-533-104A-22	Sequence 22, Appl
54	433	65.3	140	7	US-11-006-808-4	Sequence 4, Appli
55	432.5	65.2	117	6	US-10-522-086-1	Sequence 1, Appli
56	431.5	65.1	121	6	US-10-522-086-4	Sequence 4, Appli
57	430	64.9	125	7	US-11-219-563-80	Sequence 80, Appl
58	426.5	64.3	120	7	US-11-304-986-22	Sequence 22, Appl
59	426	64.3	129	7	US-11-006-808-45	Sequence 45, Appl

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This page gives you Search Results detail for the Application 10661366 and Search Result us-10-661-3... [start](#)

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OM protein - protein search, using sw model

Run on: August 9, 2006, 08:00:49 ; Search time 49.0614 Seconds
(without alignments)
245.144 Million cell updates/sec

Title: US-10-661-366-1
Perfect score: 663
Sequence: 1 QVQMQQSGAELVKPGASVKL.....GSYYYAMDYWGQGTSTVTVSS 125

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	509	76.8	123	2 F48677	Ig heavy chain V-D
2	504	76.0	123	2 E48677	Ig heavy chain V-D
3	498	75.1	140	2 PH1482	Ig heavy chain V r
4	493	74.4	123	2 G48677	Ig heavy chain V-D
5	492	74.2	246	2 S38950	Ig gamma chain - m
6	492	74.2	446	2 S40295	Ig gamma-2a chain
7	491	74.1	138	2 E32513	Ig heavy chain pre
8	482.5	72.8	131	2 S66537	Ig heavy chain V r

9	482	72.7	121	2	A26405	Ig heavy chain V r
10	482	72.7	138	2	S21810	Ig heavy chain V r
11	479.5	72.3	120	2	G28195	Ig heavy chain V r
12	477	71.9	140	2	PH1484	Ig heavy chain V r
13	477	71.9	140	2	PH1489	Ig heavy chain V r
14	476	71.8	121	2	A21854	Ig heavy chain V r
15	475.5	71.7	115	2	A54378	Ig heavy chain V r
16	475.5	71.7	139	2	PS0024	Ig heavy chain pre
17	474	71.5	118	2	S38565	Ig heavy chain V r
18	474	71.5	140	2	PH1498	Ig heavy chain V r
19	473.5	71.4	119	2	A24672	Ig heavy chain pre
20	473	71.3	135	2	PH1493	Ig heavy chain V r
21	473	71.3	140	1	HVMSG7	Ig heavy chain pre
22	470	70.9	140	2	PH1486	Ig heavy chain V r
23	469.5	70.8	120	2	F28195	Ig heavy chain V r
24	469.5	70.8	469	2	S37483	Ig gamma-2a chain
25	468	70.6	119	2	PH1520	Ig heavy chain V r
26	467	70.4	123	2	S20646	Ig heavy chain V r
27	466.5	70.4	120	2	S41394	Ig heavy chain V r
28	466.5	70.4	120	2	B22769	Ig heavy chain V r
29	466.5	70.4	122	2	S24287	Ig heavy chain V r
30	466	70.3	119	2	PH1502	Ig heavy chain V r
31	466	70.3	140	2	PH1488	Ig heavy chain V r
32	465.5	70.2	139	1	MHMS18	Ig heavy chain pre
33	465.5	70.2	287	4	PC4402	pelB leader/Ig hea
34	465	70.1	119	2	PH1521	Ig heavy chain V r
35	463	69.8	121	2	A30551	Ig heavy chain V r
36	462.5	69.8	117	2	PL0237	Ig heavy chain V r
37	462	69.7	119	2	PH1504	Ig heavy chain V r
38	462	69.7	119	2	PH1512	Ig heavy chain V r
39	462	69.7	123	2	B30560	Ig heavy chain V r
40	460	69.4	122	2	S20643	Ig heavy chain V r
41	459.5	69.3	117	2	PL0235	Ig heavy chain V r
42	459	69.2	119	2	PH1518	Ig heavy chain V r
43	459	69.2	119	2	PH1500	Ig heavy chain V r
44	457	68.9	114	2	PH1522	Ig heavy chain V r
45	456.5	68.9	115	2	PL0238	Ig heavy chain V r
46	456.5	68.9	141	2	A39276	Ig heavy chain pre
47	456	68.8	119	2	E30562	Ig heavy chain V r
48	456	68.8	135	2	PH1492	Ig heavy chain V r
49	455	68.6	125	2	S20639	Ig heavy chain V r
50	454.5	68.6	117	2	B27563	Ig heavy chain V r
51	454	68.5	117	1	HVMSA1	Ig heavy chain pre
52	454	68.5	118	2	A24754	Ig heavy chain V r
53	453.5	68.4	139	2	A27609	Ig heavy chain pre
54	453	68.3	114	2	PH1523	Ig heavy chain V r
55	453	68.3	119	2	PH1517	Ig heavy chain V r
56	452	68.2	135	2	PH1494	Ig heavy chain V r
57	452	68.2	140	2	PH1483	Ig heavy chain V r
58	451	68.0	119	2	PH1505	Ig heavy chain V r
59	450.5	67.9	118	2	S38717	Ig heavy chain V r
60	450	67.9	109	2	PH0997	Ig heavy chain V r
61	450	67.9	140	2	A36194	Ig heavy chain V r
62	449.5	67.8	133	2	PC1155	Ig heavy chain pre
63	447	67.4	109	2	PH1001	Ig heavy chain V r
64	445.5	67.2	120	2	S09956	Ig heavy chain V-D
65	445	67.1	119	2	C30562	Ig heavy chain V r
66	445	67.1	140	2	PH1499	Ig heavy chain V r
67	445	67.1	140	2	S04575	Ig heavy chain pre
68	444.5	67.0	116	2	S53751	antibody Fab Jel 1
69	444.5	67.0	117	2	PL0234	Ig heavy chain V r

SCORE Search Results Details for Application 10661366 and Search Result us-10-661-366-1.rup.

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OM protein - protein search, using sw model

Run on: August 9, 2006, 07:46:18 ; Search time 377.986 Seconds
(without alignments)
305.902 Million cell updates/sec

Title: US-10-661-366-1
Perfect score: 663
Sequence: 1 QVQMQQSGAELVKPGASVKL.....GSYYAMDYWGQGTSVTVSS 125

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	499	75.3	147	2	Q925S3_MOUSE	Q925s3 mus musculu
2	496	74.8	120	1	HV03_MOUSE	P01747 mus musculu
3	493.5	74.4	145	2	Q924R1_MOUSE	Q924r1 mus musculu
4	486	73.3	458	2	Q5BJZ2_RAT	Q5bjz2 rattus norv

5	485.5	73.2	145	2	Q924Q6_MOUSE	Q924q6	mus	musculu
6	482.5	72.8	145	2	Q924R4_MOUSE	Q924r4	mus	musculu
7	480.5	72.5	145	2	Q924P7_MOUSE	Q924p7	mus	musculu
8	478	72.1	146	2	Q924Q3_MOUSE	Q924q3	mus	musculu
9	477.5	72.0	145	2	Q924Q9_MOUSE	Q924q9	mus	musculu
10	474	71.5	473	2	Q9D8L4_MOUSE	Q9d8l4	mus	musculu
11	473	71.3	140	1	HV02_MOUSE	P01746	mus	musculu
12	472.5	71.3	463	2	Q99LC4_MOUSE	Q99lc4	mus	musculu
13	472.5	71.3	590	2	Q4V9V8_MOUSE	Q4v9v8	mus	musculu
14	472	71.2	481	2	Q91WT1_MOUSE	Q91wt1	mus	musculu
15	471.5	71.1	484	2	Q3SYJ4_MOUSE	Q3syj4	mus	musculu
16	469	70.7	146	2	Q924R8_MOUSE	Q924r8	mus	musculu
17	469	70.7	468	2	Q569W9_MOUSE	Q569w9	mus	musculu
18	467.5	70.5	617	2	Q4KML5_MOUSE	Q4kml5	mus	musculu
19	465.5	70.2	139	1	HV07_MOUSE	P01751	mus	musculu
20	465.5	70.2	145	2	Q924Q7_MOUSE	Q924q7	mus	musculu
21	464.5	70.1	143	2	Q924R0_MOUSE	Q924r0	mus	musculu
22	464	70.0	614	2	Q7TMT6_MOUSE	Q7tmt6	mus	musculu
23	460	69.4	142	2	Q924Q1_MOUSE	Q924q1	mus	musculu
24	459.5	69.3	143	2	Q924Q0_MOUSE	Q924q0	mus	musculu
25	459.5	69.3	482	2	Q8K172_MOUSE	Q8k172	mus	musculu
26	458	69.1	140	2	Q924R2_MOUSE	Q924r2	mus	musculu
27	457.5	69.0	145	2	Q924R3_MOUSE	Q924r3	mus	musculu
28	457	68.9	480	2	Q8K0Z4_MOUSE	Q8k0z4	mus	musculu
29	454.5	68.6	465	2	Q6PJB2_MOUSE	Q6pjb2	mus	musculu
30	454	68.5	117	1	HV52_MOUSE	P06327	mus	musculu
31	454	68.5	479	2	Q3KQK2_MOUSE	Q3kqk2	mus	musculu
32	449	67.7	616	2	Q504M7_MOUSE	Q504m7	mus	musculu
33	447	67.4	489	2	Q8VCX4_MOUSE	Q8vcx4	mus	musculu
34	446.5	67.3	143	2	Q924P9_MOUSE	Q924p9	mus	musculu
35	446	67.3	144	2	Q924P5_MOUSE	Q924p5	mus	musculu
36	444	67.0	117	2	Q9QXE9_MOUSE	Q9qxe9	mus	musculu
37	444	67.0	142	2	Q924Q2_MOUSE	Q924q2	mus	musculu
38	444	67.0	464	2	Q6PF95_MOUSE	Q6pf95	mus	musculu
39	443.5	66.9	143	2	Q924Q5_MOUSE	Q924q5	mus	musculu
40	442.5	66.7	137	2	Q924R6_MOUSE	Q924r6	mus	musculu
41	442	66.7	146	2	Q924Q8_MOUSE	Q924q8	mus	musculu
42	441.5	66.6	118	2	Q9Z1C4_MOUSE	Q9z1c4	mus	musculu
43	441.5	66.6	141	2	Q924Q4_MOUSE	Q924q4	mus	musculu
44	441.5	66.6	143	2	Q924R7_MOUSE	Q924r7	mus	musculu
45	440.5	66.4	613	2	Q8VCX7_MOUSE	Q8vcx7	mus	musculu
46	439	66.2	475	2	Q5FVP3_RAT	Q5fvp3	rattus	norv
47	438.5	66.1	487	2	Q65ZL2_9MURI	Q65zl2	mus	sp. fv/
48	438.5	66.1	488	2	Q8K0F2_MOUSE	Q8k0f2	mus	musculu
49	437	65.9	134	2	Q65ZR6_MOUSE	Q65zr6	mus	musculu
50	437	65.9	598	2	Q568Y0_RAT	Q568y0	rattus	norv
51	436.5	65.8	143	2	Q91VA2_MOUSE	Q91va2	mus	musculu
52	435.5	65.7	484	2	Q3KQK0_MOUSE	Q3kqk0	mus	musculu
53	435.5	65.7	591	2	Q4QQW0_RAT	Q4qqw0	rattus	norv
54	435	65.6	140	2	Q924P8_MOUSE	Q924p8	mus	musculu
55	434.5	65.5	482	2	Q2T9K9_MOUSE	Q2t9k9	mus	musculu
56	434	65.5	470	2	Q7TMK1_MOUSE	Q7tmk1	mus	musculu
57	431	65.0	170	2	Q925S2_MOUSE	Q925s2	mus	musculu
58	431	65.0	468	2	Q505N9_MOUSE	Q505n9	mus	musculu
59	431	65.0	483	2	Q52L51_MOUSE	Q52l51	mus	musculu
60	430.5	64.9	137	1	HV11_MOUSE	P01755	mus	musculu
61	430	64.9	121	1	HV01_MOUSE	P01745	mus	musculu
62	427	64.4	117	2	Q9QXF0_MOUSE	Q9qxf0	mus	musculu
63	427	64.4	472	2	Q6PJA7_MOUSE	Q6pja7	mus	musculu
64	426.5	64.3	109	2	Q9JL75_MOUSE	Q9jl75	mus	musculu
65	426	64.3	120	2	Q5F2I1_MOUSE	Q5f2i1	mus	musculu

SCORE Search Results Details for Application 10661366 and Search Result us-10-661-366-2.rag.

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OM protein - protein search, using sw model

Run on: August 9, 2006, 07:45:18 ; Search time 270.239 Seconds
(without alignments)
181.033 Million cell updates/sec

Title: US-10-661-366-2
Perfect score: 549
Sequence: 1 QIVLTQSPAIMASLGEET.....HQWSSYPRTFGGGTKLEIKR 107

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : A_Geneseq_8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	549	100.0	107	9	ADY75167	Ady75167 Antibody
2	522	95.1	106	8	ADU39964	Adu39964 Antibody
3	521	94.9	113	4	AAB48936	Aab48936 Anti-TrkA
4	521	94.9	295	4	AAB48934	Aab48934 Anti-TrkA
5	519	94.5	106	9	AEB12544	Aeb12544 Antibody
6	511	93.1	107	2	AAR88110	Aar88110 Murine an
7	511	93.1	129	2	AAR88108	Aar88108 Murine an
8	506	92.2	107	9	AEB70882	Aeb70882 Toll-like
9	498.5	90.8	212	6	ABP70661	Abp70661 Murine in
10	493	89.8	104	8	ADL11889	Adl11889 Chimera a
11	493	89.8	104	9	ADZ58533	Adz58533 VEGF rece
12	493	89.8	126	3	AAV77594	Aay77594 Anti-huma
13	493	89.8	126	4	AAB78863	Aab78863 Anti-huma
14	487.5	88.8	100	2	AAR07319	Aar07319 VK domain
15	487.5	88.8	100	2	AAW14487	Aawl4487 Monoclona
16	487.5	88.8	100	2	AAR99876	Aar99876 Monoclona
17	455	82.9	108	8	ADT74993	Adt74993 Light cha
18	453	82.5	122	2	AAR25958	Aar25958 ICAM-1 in
19	453	82.5	129	10	AEF76249	Aef76249 Prostate
20	452	82.3	106	10	AEF51045	Aef51045 Variable
21	451	82.1	108	8	ADE25838	Ade25838 Anti-alph
22	451	82.1	108	8	ADE25837	Ade25837 Anti-alph
23	450	82.0	106	8	ADU86522	Adu86522 Immunoglo
24	450	82.0	106	8	ADU86521	Adu86521 Immunoglo
25	450	82.0	107	4	AAB83159	Aab83159 Mouse gan
26	450	82.0	107	9	ADZ52586	Adz52586 Mouse ant
27	450	82.0	109	9	AED10367	Aed10367 Anti-myos
28	450	82.0	129	2	AAR53329	Aar53329 KM-796 an
29	450	82.0	129	2	AAV28385	Aay28385 Anti-GM2
30	450	82.0	129	2	AAV28357	Aay28357 Antibody
31	449	81.8	106	8	ADO16879	Ado16879 Murine an
32	449	81.8	128	2	AAR90690	Aar90690 Mouse 5C7
33	449	81.8	129	5	ABB75616	Abb75616 Anti-RANK
34	448	81.6	109	9	AED10360	Aed10360 Anti-myos
35	448	81.6	129	9	ADZ81865	Adz81865 Anti-lami
36	447	81.4	109	9	AED10361	Aed10361 Anti-myos
37	447	81.4	129	10	AEF76256	Aef76256 Prostate
38	446	81.2	108	9	AEA89805	Aea89805 Antibody
39	446	81.2	108	9	AEA44098	Aea44098 Anti-TPO
40	446	81.2	128	2	AAR12327	Aar12327 Light (ka
41	446	81.2	236	2	AAV34096	Aay34096 Partial a
42	446	81.2	255	8	ADS14282	Adsl4282 Murine pr
43	446	81.2	519	8	ADS14288	Adsl4288 Murine pr
44	445	81.1	106	2	AAR24105	Aar24105 Anti-Tac
45	445	81.1	106	2	AAW58511	Aaw58511 Protein S
46	445	81.1	106	4	AAB69651	Aab69651 Murine an
47	445	81.1	106	4	AAB69641	Aab69641 Murine an
48	445	81.1	106	8	ADI01224	Adi01224 Protein s
49	445	81.1	106	8	ADO47704	Ado47704 Mouse ant
50	445	81.1	128	1	AAP93150	Aap93150 Protein e
51	445	81.1	128	6	ABJ39021	Abj39021 Murine an
52	445	81.1	239	3	AAB12563	Aab12563 Anti-TAC
53	445	81.1	239	4	AAB36826	Aab36826 Anti-TAC
54	445	81.1	438	6	ABJ39019	Abj39019 Anti-TAC
55	445	81.1	599	2	AAW37132	Aaw37132 Anti-Tac(
56	445	81.1	599	2	AAW95462	Aaw95462 Anti-Tac(
57	445	81.1	599	3	AAV87477	Aay87477 Anti-Tac(

SCORE Search Results Details for Application 10661366 and Search Result us-10-661-366- 2.ra1.

Score Home	Retrieve Application	SCORE System	SCORE	Comments /
Page	List	Overview	FAQ	Suggestions

This page gives you Search Results detail for the Application 10661366 and Search Result us-10-661-366-2.ra1.

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OM protein - protein search, using sw model

Run on: August 9, 2006, 08:17:00 ; Search time 70.4812 Seconds
(without alignments)
132.883 Million cell updates/sec

Title: US-10-661-366-2
Perfect score: 549
Sequence: 1 QIVLTQSPAIMSASLGEEIT.....HQWSSYPRTFGGGTKLEIKR 107

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Issued_Patents_AA:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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No.	Score	Match Length DB ID
		Description

1	511	93.1	129	5	PCT-US95-07372-12	Sequence 12, Appl
2	498	90.7	105	2	US-09-453-718B-108	Sequence 108, App
3	493	89.8	104	2	US-09-453-718B-100	Sequence 100, App
4	493	89.8	126	2	US-09-453-718B-89	Sequence 89, Appl
5	487.5	88.8	100	1	US-08-308-494A-15	Sequence 15, Appl
6	450	82.0	129	1	US-08-116-778E-2	Sequence 2, Appli
7	450	82.0	129	1	US-08-438-562-2	Sequence 2, Appli
8	450	82.0	129	1	US-08-483-528B-92	Sequence 92, Appl
9	449	81.8	128	2	US-08-619-491-2	Sequence 2, Appli
10	449	81.8	128	5	PCT-US95-07302-2	Sequence 2, Appli
11	445	81.1	106	1	US-07-634-278-1	Sequence 1, Appli
12	445	81.1	106	1	US-07-634-278-16	Sequence 16, Appl
13	445	81.1	106	1	US-08-477-728-1	Sequence 1, Appli
14	445	81.1	106	1	US-08-477-728-16	Sequence 16, Appl
15	445	81.1	106	1	US-08-474-040-1	Sequence 1, Appli
16	445	81.1	106	1	US-08-474-040-16	Sequence 16, Appl
17	445	81.1	106	1	US-08-487-200-1	Sequence 1, Appli
18	445	81.1	106	1	US-08-487-200-16	Sequence 16, Appl
19	445	81.1	106	1	US-08-488-113B-163	Sequence 163, App
20	445	81.1	106	1	US-08-477-484B-163	Sequence 163, App
21	445	81.1	106	1	US-08-107-669D-49	Sequence 49, Appl
22	445	81.1	106	1	US-08-472-788A-83	Sequence 83, Appl
23	445	81.1	106	1	US-08-477-531B-49	Sequence 49, Appl
24	445	81.1	106	1	US-08-646-360-163	Sequence 163, App
25	445	81.1	106	1	US-08-082-842A-83	Sequence 83, Appl
26	445	81.1	106	2	US-08-839-765-163	Sequence 163, App
27	445	81.1	106	2	US-09-136-389-163	Sequence 163, App
28	445	81.1	106	2	US-08-484-537-1	Sequence 1, Appli
29	445	81.1	106	2	US-08-484-537-16	Sequence 16, Appl
30	445	81.1	106	2	US-09-610-838-163	Sequence 163, App
31	445	81.1	106	2	US-09-711-485-163	Sequence 163, App
32	445	81.1	106	3	US-09-718-998-1	Sequence 1, Appli
33	445	81.1	106	3	US-09-718-998-16	Sequence 16, Appl
34	445	81.1	239	2	US-08-279-772A-8	Sequence 8, Appli
35	445	81.1	239	2	US-08-902-486-11	Sequence 11, Appl
36	445	81.1	599	1	US-08-463-163-3	Sequence 3, Appli
37	439.5	80.1	110	2	US-08-836-561-33	Sequence 33, Appl
38	439.5	80.1	110	2	US-09-434-122-33	Sequence 33, Appl
39	438	79.8	108	2	US-09-726-219A-243	Sequence 243, App
40	438	79.8	108	2	US-09-196-522-243	Sequence 243, App
41	438	79.8	222	1	US-08-190-199A-67	Sequence 67, Appl
42	438	79.8	235	1	US-08-190-199A-61	Sequence 61, Appl
43	438	79.8	281	2	US-09-423-439-44	Sequence 44, Appl
44	438	79.8	666	2	US-09-423-439-51	Sequence 51, Appl
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46	437	79.6	106	1	US-08-477-728-58	Sequence 58, Appl
47	437	79.6	106	1	US-08-474-040-58	Sequence 58, Appl
48	437	79.6	106	1	US-08-487-200-58	Sequence 58, Appl
49	437	79.6	106	2	US-08-484-537-58	Sequence 58, Appl
50	437	79.6	106	3	US-09-718-998-58	Sequence 58, Appl
51	437	79.6	128	1	US-07-634-278-31	Sequence 31, Appl
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53	437	79.6	128	1	US-08-474-040-31	Sequence 31, Appl
54	437	79.6	128	1	US-08-487-200-31	Sequence 31, Appl
55	437	79.6	128	2	US-08-484-537-31	Sequence 31, Appl
56	437	79.6	128	3	US-09-718-998-31	Sequence 31, Appl
57	437	79.6	244	1	US-08-553-497A-20	Sequence 20, Appl
58	436	79.4	105	2	US-08-434-000A-12	Sequence 12, Appl
59	436	79.4	105	2	US-09-312-157-12	Sequence 12, Appl
60	436	79.4	105	2	US-09-717-888-12	Sequence 12, Appl

SCORE Search Results Details for Application 10661366 and Search Result us-10-661-366-2.rapbm.

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OM protein - protein search, using sw model

Run on: August 9, 2006, 09:01:05 ; Search time 228.973 Seconds
(without alignments)
216.462 Million cell updates/sec

Title: US-10-661-366-2
Perfect score: 549
Sequence: 1 QIVLTQSPAIMSASLGEEIT.....HQWSSYPRTFGGGTKLEIKR 107

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Published_Applications_AA_Main:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%	Query					
No.	Score	Match	Length	DB	ID	Description	

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3	504	91.8	107	6	US-11-009-939-7	Sequence 7, Appli
4	498	90.7	105	6	US-11-250-411-108	Sequence 108, App
5	493	89.8	104	6	US-11-250-411-100	Sequence 100, App
6	493	89.8	126	4	US-10-160-232-89	Sequence 89, Appl
7	493	89.8	126	6	US-11-250-411-89	Sequence 89, Appl
8	455	82.9	108	6	US-11-097-812-39	Sequence 39, Appl
9	451	82.1	108	5	US-10-507-662-44	Sequence 44, Appl
10	451	82.1	108	5	US-10-507-662-45	Sequence 45, Appl
11	449	81.8	129	4	US-10-344-779-2	Sequence 2, Appli
12	449	81.8	129	4	US-10-738-809-2	Sequence 2, Appli
13	445	81.1	106	4	US-10-127-890-163	Sequence 163, App
14	445	81.1	106	4	US-10-340-189-83	Sequence 83, Appl
15	445	81.1	106	4	US-10-389-155-1	Sequence 1, Appli
16	445	81.1	106	4	US-10-325-696-49	Sequence 49, Appl
17	445	81.1	106	4	US-10-389-417-1	Sequence 1, Appli
18	445	81.1	106	4	US-10-452-357-1	Sequence 1, Appli
19	445	81.1	106	4	US-10-452-357-16	Sequence 16, Appl
20	445	81.1	106	5	US-10-717-243-163	Sequence 163, App
21	445	81.1	106	6	US-11-133-775-49	Sequence 49, Appl
22	445	81.1	107	3	US-09-144-886-90	Sequence 90, Appl
23	445	81.1	128	4	US-10-244-821-92	Sequence 92, Appl
24	445	81.1	438	4	US-10-244-821-88	Sequence 88, Appl
25	444	80.9	109	4	US-10-251-085B-273	Sequence 273, App
26	444	80.9	109	4	US-10-312-316-50	Sequence 50, Appl
27	444	80.9	109	4	US-10-737-252-273	Sequence 273, App
28	443	80.7	106	5	US-10-507-662-43	Sequence 43, Appl
29	443	80.7	109	4	US-10-461-878-12	Sequence 12, Appl
30	443	80.7	109	5	US-10-461-885-12	Sequence 12, Appl
31	443	80.7	215	4	US-10-410-907A-34	Sequence 34, Appl
32	442	80.5	108	4	US-10-461-878-9	Sequence 9, Appli
33	442	80.5	108	4	US-10-461-878-14	Sequence 14, Appl
34	442	80.5	108	5	US-10-461-885-9	Sequence 9, Appli
35	441	80.3	110	6	US-11-097-812-104	Sequence 104, App
36	441	80.3	242	4	US-10-259-087A-20	Sequence 20, Appl
37	441	80.3	242	4	US-10-689-006-20	Sequence 20, Appl
38	441	80.3	669	3	US-09-807-721-2	Sequence 2, Appli
39	440	80.1	109	4	US-10-251-085B-272	Sequence 272, App
40	440	80.1	109	4	US-10-737-252-272	Sequence 272, App
41	440	80.1	269	6	US-11-224-726-1	Sequence 1, Appli
42	439.5	80.1	110	4	US-10-283-349-33	Sequence 33, Appl
43	439.5	80.1	110	6	US-11-193-512-33	Sequence 33, Appl
44	439	80.0	107	3	US-09-144-886-78	Sequence 78, Appl
45	438	79.8	108	4	US-10-251-215-52	Sequence 52, Appl
46	438	79.8	108	4	US-10-803-622-243	Sequence 243, App
47	438	79.8	108	4	US-10-803-653-243	Sequence 243, App
48	438	79.8	110	6	US-11-097-812-96	Sequence 96, Appl
49	438	79.8	110	6	US-11-097-812-114	Sequence 114, App
50	437	79.6	106	4	US-10-389-155-17	Sequence 17, Appl
51	437	79.6	106	4	US-10-389-417-17	Sequence 17, Appl
52	437	79.6	106	4	US-10-452-357-58	Sequence 58, Appl
53	437	79.6	128	4	US-10-452-357-31	Sequence 31, Appl
54	437	79.6	130	3	US-09-791-551-50	Sequence 50, Appl
55	437	79.6	510	4	US-10-108-511-5	Sequence 5, Appli
56	437	79.6	510	5	US-10-482-532-5	Sequence 5, Appli
57	436.5	79.5	108	5	US-10-895-135-47	Sequence 47, Appl
58	436	79.4	105	3	US-09-982-107-12	Sequence 12, Appl
59	436	79.4	105	5	US-10-781-989-12	Sequence 12, Appl
60	436	79.4	106	6	US-11-003-819-6	Sequence 6, Appli
61	436	79.4	106	6	US-11-250-411-98	Sequence 98, Appl

SCORE Search Results Details for Application 10661366 and Search Result us-10-661-366-2.rapbn.

Score Home	Retrieve Application	SCORE System	SCORE	Comments /
Page	List	Overview	FAQ	Suggestions

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OM protein - protein search, using sw model

Run on: August 9, 2006, 09:02:15 ; Search time 35.058 Seconds
(without alignments)
205.442 Million cell updates/sec

Title: US-10-661-366-2
Perfect score: 549
Sequence: 1 QIVLTQSPAIMASLGEIT.....HQWSSYPRTFGGGTKLEIKR 107

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 239914 seqs, 67312017 residues

Total number of hits satisfying chosen parameters: 239914

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Published_Applications_AA_New:*

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- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	441	80.3	242	7	US-11-183-325-20	Sequence 20, Appl
3	438	79.8	106	6	US-10-542-682-18	Sequence 18, Appl
4	436	79.4	128	7	US-11-321-444-6	Sequence 6, Appli
5	433	78.9	110	6	US-10-514-516-6	Sequence 6, Appli
6	433	78.9	605	6	US-10-514-516-2	Sequence 2, Appli
7	430	78.3	118	6	US-10-513-539A-8	Sequence 8, Appli
8	426	77.6	106	6	US-10-542-682-17	Sequence 17, Appl
9	424	77.2	213	6	US-10-822-231-3	Sequence 3, Appli
10	424	77.2	213	7	US-11-174-287-6	Sequence 6, Appli
11	424	77.2	213	7	US-11-256-060-16	Sequence 16, Appl
12	423	77.0	128	7	US-11-315-067-4	Sequence 4, Appli
13	423	77.0	128	7	US-11-315-067-6	Sequence 6, Appli
14	420	76.5	109	7	US-11-376-338-8	Sequence 8, Appli
15	419	76.3	106	7	US-11-256-060-1	Sequence 1, Appli
16	419	76.3	128	7	US-11-183-218-60	Sequence 60, Appl
17	418	76.1	106	6	US-10-542-682-15	Sequence 15, Appl
18	418	76.1	106	6	US-10-542-682-16	Sequence 16, Appl
19	418	76.1	107	7	US-11-254-182-25	Sequence 25, Appl
20	418	76.1	107	7	US-11-106-762-17	Sequence 17, Appl
21	418	76.1	107	7	US-11-238-281-1	Sequence 1, Appli
22	418	76.1	107	7	US-11-291-698A-41	Sequence 41, Appl
23	414	75.4	128	7	US-11-321-444-8	Sequence 8, Appli
24	412	75.0	108	6	US-10-522-086-5	Sequence 5, Appli
25	412	75.0	129	6	US-10-513-148A-4	Sequence 4, Appli
26	410.5	74.8	128	6	US-10-528-928-10	Sequence 10, Appl
27	410	74.7	118	6	US-10-513-539A-4	Sequence 4, Appli
28	407	74.1	242	7	US-11-183-325-18	Sequence 18, Appl
29	403.5	73.5	120	7	US-11-315-067-37	Sequence 37, Appl
30	393.5	71.7	120	7	US-11-315-067-36	Sequence 36, Appl
31	392	71.4	106	7	US-11-301-373-46	Sequence 46, Appl
32	390	71.0	213	7	US-11-263-230-231	Sequence 231, App
33	387	70.5	213	7	US-11-263-230-211	Sequence 211, App
34	385	70.1	106	7	US-11-263-230-54	Sequence 54, Appl
35	385	70.1	213	7	US-11-263-230-255	Sequence 255, App
36	384	69.9	213	7	US-11-263-230-233	Sequence 233, App
37	384	69.9	213	7	US-11-263-230-239	Sequence 239, App
38	384	69.9	213	7	US-11-263-230-247	Sequence 247, App
39	382	69.6	106	7	US-11-263-230-13	Sequence 13, Appl
40	382	69.6	213	7	US-11-263-230-241	Sequence 241, App
41	381	69.4	107	7	US-11-254-182-26	Sequence 26, Appl
42	381	69.4	107	7	US-11-106-762-1	Sequence 1, Appli
43	381	69.4	107	7	US-11-106-762-18	Sequence 18, Appl
44	381	69.4	107	7	US-11-238-281-2	Sequence 2, Appli
45	381	69.4	107	7	US-11-291-698A-42	Sequence 42, Appl
46	381	69.4	213	7	US-11-254-182-63	Sequence 63, Appl
47	381	69.4	213	7	US-11-106-762-3	Sequence 3, Appli
48	381	69.4	213	7	US-11-106-762-24	Sequence 24, Appl
49	381	69.4	213	7	US-11-238-281-13	Sequence 13, Appl
50	381	69.4	232	7	US-11-106-762-23	Sequence 23, Appl
51	381	69.4	232	7	US-11-291-698A-56	Sequence 56, Appl
52	380	69.2	106	7	US-11-263-230-11	Sequence 11, Appl
53	380	69.2	213	7	US-11-263-230-237	Sequence 237, App
54	380	69.2	213	7	US-11-263-230-243	Sequence 243, App
55	379	69.0	106	7	US-11-263-230-56	Sequence 56, Appl
56	379	69.0	106	7	US-11-263-230-65	Sequence 65, Appl
57	379	69.0	213	7	US-11-263-230-245	Sequence 245, App
58	377	68.7	106	7	US-11-263-230-60	Sequence 60, Appl
59	377	68.7	213	7	US-11-263-230-333	Sequence 333, App

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OM protein - protein search, using sw model

Run on: August 9, 2006, 08:00:49 ; Search time 41.9966 Seconds
(without alignments)
245.144 Million cell updates/sec

Title: US-10-661-366-2
Perfect score: 549
Sequence: 1 QIVLTQSPAIMSASLGEEIT.....HQWSSYPRTFGGGTKLEIKR 107

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	455	82.9	107	2	A30562	Ig kappa chain V r
2	454	82.7	107	2	B30562	Ig kappa chain V r
3	452	82.3	94	2	S20653	Ig heavy chain V r
4	448	81.6	94	2	S20650	Ig heavy chain V r
5	439	80.0	130	1	JL0079	Ig kappa chain pre
6	438	79.8	235	2	S25058	Ig kappa chain - m
7	437	79.6	140	2	PL0013	Ig kappa chain pre
8	434	79.1	105	2	S26338	Ig kappa chain V r

9	433	78.9	106	2	PS0071	Ig kappa chain V r
10	433	78.9	107	2	PT0406	Ig kappa chain V r
11	431	78.5	104	2	B49049	Ig kappa chain V r
12	430	78.3	103	2	S29591	Ig kappa chain V r
13	429	78.1	106	2	G27887	Ig kappa chain V r
14	429	78.1	130	2	A32513	Ig kappa chain pre
15	427	77.8	107	2	PC4405	Ig kappa chain V r
16	426	77.6	107	2	S11119	Ig kappa chain V r
17	424.5	77.3	108	2	G30560	Ig kappa chain V r
18	424	77.2	106	2	B54378	Ig light chain V r
19	421	76.7	100	2	S29590	Ig kappa chain V r
20	421	76.7	107	2	S11118	Ig kappa chain V r
21	419	76.3	107	1	KVMSX4	Ig kappa chain V r
22	419	76.3	107	2	A42848	Ig light chain V r
23	419	76.3	130	2	S04573	Ig kappa chain pre
24	418	76.1	106	2	PL0082	Ig kappa chain V r
25	418	76.1	107	2	S11121	Ig kappa chain V r
26	417	76.0	104	2	JC6076	anti-D-dimer monoc
27	416	75.8	129	1	KVMS7B	Ig kappa chain pre
28	415.5	75.7	108	2	S38720	Ig light chain V r
29	415	75.6	130	2	B32456	Ig kappa chain pre
30	414	75.4	113	2	S03410	Ig kappa chain pre
31	412	75.0	107	2	PT0402	Ig light chain V r
32	411	74.9	120	2	A34871	Ig kappa chain V r
33	410	74.7	123	2	S05269	Ig kappa chain pre
34	409	74.5	107	2	S11117	Ig kappa chain V r
35	408	74.3	108	2	S29581	Ig kappa chain V r
36	407	74.1	107	2	S11112	Ig kappa chain V r
37	407	74.1	108	2	PL0278	Ig kappa chain V r
38	407	74.1	132	2	S05268	Ig kappa chain pre
39	406	74.0	109	2	PT0405	Ig light chain V r
40	405	73.8	107	2	PD0011	Ig kappa chain V r
41	405	73.8	107	2	PT0398	Ig light chain V r
42	404	73.6	97	2	PH1084	Ig light chain V r
43	404	73.6	107	2	PT0403	Ig light chain V r
44	403	73.4	108	2	PL0277	Ig kappa chain V r
45	403	73.4	108	2	PL0276	Ig kappa chain V r
46	401.5	73.1	98	2	PH1061	Ig light chain V r
47	401	73.0	96	2	C33730	Ig kappa chain V r
48	401	73.0	99	2	S29585	Ig kappa chain V r
49	401	73.0	106	2	PS0070	Ig kappa chain V r
50	401	73.0	120	2	S66536	Ig light chain V r
51	400	72.9	97	2	S26341	Ig light chain V r
52	399	72.7	109	2	S13699	Ig kappa chain V r
53	399	72.7	124	2	S05267	Ig kappa chain pre
54	397	72.3	108	2	PS0069	Ig kappa chain V r
55	396.5	72.2	106	2	S11114	Ig kappa chain V r
56	396	72.1	107	2	PT0401	Ig light chain V r
57	394	71.8	95	2	D33730	Ig kappa chain V r
58	394	71.8	99	2	PH1058	Ig light chain V r
59	394	71.8	107	2	S11113	Ig kappa chain V r
60	393	71.6	106	2	S29583	Ig kappa chain V r
61	393	71.6	107	1	KVMSJ5	Ig kappa chain V r
62	393	71.6	109	2	PT0404	Ig light chain V r
63	392	71.4	107	2	PT0397	Ig light chain V r
64	391	71.2	99	2	D38601	Ig kappa chain V r
65	391	71.2	107	2	PT0400	Ig light chain V r
66	390	71.0	107	2	PT0395	Ig light chain V r
67	388	70.7	97	2	PH1085	Ig light chain V r
68	388	70.7	102	2	S29584	Ig kappa chain V r
69	387	70.5	99	2	PH1059	Ig light chain V r

SCORE Search Results Details for Application 10661366 and Search Result us-10-661-366-2.rup.

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OM protein - protein search, using sw model

Run on: August 9, 2006, 07:46:18 ; Search time 323.556 Seconds
(without alignments)
305.902 Million cell updates/sec

Title: US-10-661-366-2
Perfect score: 549
Sequence: 1 QIVLTQSPAIMSASLGEEIT.....HQWSSYPRTFGGGTKLEIKR 107

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	451	82.1	134	2	Q8VDD0_MOUSE	Q8vdd0 mus musculu
2	442	80.5	114	2	Q8K1F1_MOUSE	Q8klf1 mus musculu
3	439	80.0	112	2	Q8K1F3_MOUSE	Q8klf3 mus musculu
4	437	79.6	235	2	Q58EV6_MOUSE	Q58ev6 mus musculu

5	436	79.4	112	2	Q8K1F0_MOUSE	Q8k1f0	mus	musculu
6	434	79.1	112	2	Q8K1F2_MOUSE	Q8k1f2	mus	musculu
7	432	78.7	107	1	KV6F_MOUSE	P04940	mus	musculu
8	428	78.0	106	2	Q2VT27_MOUSE	Q2vt27	mus	musculu
9	427	77.8	107	1	KV6I_MOUSE	P04943	mus	musculu
10	426	77.6	106	2	Q2VR04_MOUSE	Q2vr04	mus	musculu
11	426	77.6	107	1	KV6H_MOUSE	P04942	mus	musculu
12	424	77.2	106	2	Q9U410_MOUSE	Q9u410	mus	musculu
13	423	77.0	107	1	KV6G_MOUSE	P04941	mus	musculu
14	422	76.9	107	1	KV6J_MOUSE	P04944	mus	musculu
15	422	76.9	108	1	KV6K_MOUSE	P04945	mus	musculu
16	419	76.3	107	1	KV6A_MOUSE	P01675	mus	musculu
17	419	76.3	107	1	KV6D_MOUSE	P01678	mus	musculu
18	417	76.0	237	2	Q569Y8_MOUSE	Q569y8	mus	musculu
19	416	75.8	129	1	KV4A_MOUSE	P01680	mus	musculu
20	413	75.2	106	2	Q2VT25_MOUSE	Q2vt25	mus	musculu
21	413	75.2	107	1	KV6B_MOUSE	P01676	mus	musculu
22	411	74.9	107	1	KV6C_MOUSE	P01677	mus	musculu
23	410	74.7	106	2	Q2VT29_MOUSE	Q2vt29	mus	musculu
24	408	74.3	235	2	Q5XFY8_MOUSE	Q5xfy8	mus	musculu
25	405.5	73.9	131	2	Q811C3_MOUSE	Q811c3	mus	musculu
26	401	73.0	237	2	Q3KQK1_MOUSE	Q3kqk1	mus	musculu
27	393	71.6	107	1	KV6E_MOUSE	P01679	mus	musculu
28	380.5	69.3	97	2	Q9JL76_MOUSE	Q9jl76	mus	musculu
29	366.5	66.8	101	2	Q9JL78_MOUSE	Q9jl78	mus	musculu
30	358.5	65.3	244	2	Q65ZC8_HUMAN	Q65zc8	homo	sapien
31	354.5	64.6	236	2	Q6PIH7_HUMAN	Q6pih7	homo	sapien
32	354.5	64.6	236	2	Q7TS98_MOUSE	Q7ts98	mus	musculu
33	353.5	64.4	236	2	Q6PIT5_HUMAN	Q6pit5	homo	sapien
34	353.5	64.4	240	2	Q65ZC9_HUMAN	Q65zc9	homo	sapien
35	350.5	63.8	108	2	Q9UL70_HUMAN	Q9ul70	homo	sapien
36	349.5	63.7	108	1	KV5J_MOUSE	P01643	mus	musculu
37	349.5	63.7	111	1	KV3R_MOUSE	P01670	mus	musculu
38	349.5	63.7	136	1	KV5B_MOUSE	P01634	mus	musculu
39	348.5	63.5	111	1	KV3L_MOUSE	P01664	mus	musculu
40	348.5	63.5	236	2	Q6GMX9_HUMAN	Q6gmx9	homo	sapien
41	347.5	63.3	111	2	Q811U6_MOUSE	Q811u6	mus	musculu
42	346.5	63.1	111	1	KV3O_MOUSE	P01667	mus	musculu
43	346	63.0	109	2	Q9UL78_HUMAN	Q9ul78	homo	sapien
44	345.5	62.9	108	2	Q9UL79_HUMAN	Q9ul79	homo	sapien
45	345.5	62.9	109	2	Q920E6_MOUSE	Q920e6	mus	musculu
46	342.5	62.4	111	1	KV3J_MOUSE	P01662	mus	musculu
47	342.5	62.4	111	2	Q920E9_MOUSE	Q920e9	mus	musculu
48	342.5	62.4	234	2	Q4KM66_RAT	Q4km66	rattus	norv
49	342	62.3	110	1	KV3P_MOUSE	P01668	mus	musculu
50	341.5	62.2	108	1	KV1P_HUMAN	P01608	homo	sapien
51	341.5	62.2	108	1	KV5K_MOUSE	P01644	mus	musculu
52	341.5	62.2	111	1	KV3M_MOUSE	P01665	mus	musculu
53	341.5	62.2	131	1	KV3I_MOUSE	P01661	mus	musculu
54	340.5	62.0	108	1	KV1S_HUMAN	P01611	homo	sapien
55	340.5	62.0	111	1	KV3N_MOUSE	P01666	mus	musculu
56	340.5	62.0	234	2	Q5M838_RAT	Q5m838	rattus	norv
57	340.5	62.0	236	2	Q6GMX8_HUMAN	Q6gmx8	homo	sapien
58	340	61.9	107	2	Q96SA9_HUMAN	Q96sa9	homo	sapien
59	340	61.9	129	1	KV3L_HUMAN	P18135	homo	sapien
60	339.5	61.8	108	1	KV1B_HUMAN	P01594	homo	sapien
61	339.5	61.8	111	1	KV3H_MOUSE	P01660	mus	musculu
62	339	61.7	239	2	Q5HZC6_XENTR	Q5hzc6	xenopus	tro
63	338.5	61.7	108	1	KV1V_HUMAN	P04430	homo	sapien
64	338.5	61.7	111	1	KV3T_MOUSE	P01672	mus	musculu
65	338.5	61.7	189	2	Q569I7_HUMAN	Q569i7	homo	sapien

SCORE Search Results Details for Application 10661366 and Search Result us-10-661-366-3.closed.rag.

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OM protein - protein search, using sw model

Run on: August 9, 2006, 06:40:12 ; Search time 92.9508 Seconds
(without alignments)
49.189 Million cell updates/sec

Title: US-10-661-366-3
Perfect score: 44
Sequence: 1 SASSSVSYML 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 837128

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Database : A_Geneseq_8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	44	100.0	10	9	ADY75168	Ady75168 Antibody
2	40	90.9	10	2	AAW27424	Aaw27424 CDR1 from
3	40	90.9	10	2	AAW73169	Aaw73169 CDR1 of 1
4	40	90.9	10	2	AAY28390	Aay28390 Peptide f
5	40	90.9	10	3	AAY77582	Aay77582 Anti-huma
6	40	90.9	10	3	AAY77588	Aay77588 Anti-huma
7	40	90.9	10	3	AAY97232	Aay97232 Complemen
8	40	90.9	10	4	AAB82706	Aab82706 VEGF anta
9	40	90.9	10	4	AAE13140	Aae13140 Humanised
10	40	90.9	10	4	AAB83163	Aab83163 Mouse gan
11	40	90.9	10	4	AAB78857	Aab78857 Anti-huma
12	40	90.9	10	4	AAB78851	Aab78851 Anti-huma
13	40	90.9	10	5	AAU81247	Aau81247 Murine tr
14	40	90.9	10	5	AAE25952	Aae25952 Mouse ant
15	40	90.9	10	5	AAU74409	Aau74409 Light cha
16	40	90.9	10	5	AAU70361	Aau70361 Mouse Kap
17	40	90.9	10	5	ABB75618	Abb75618 Anti-RANK
18	40	90.9	10	6	ABJ26721	Abj26721 VEGF bind
19	40	90.9	10	8	ADE85698	Ade85698 Human Eph
20	40	90.9	10	8	ADH77348	Adh77348 Yeast kil
21	40	90.9	10	8	ADH77354	Adh77354 Yeast kil
22	40	90.9	10	8	ADL11883	Adl11883 CDR-1 lig
23	40	90.9	10	8	ADL11880	Adl11880 CDR-1 lig
24	40	90.9	10	8	ADK18198	Adk18198 Mouse VEG
25	40	90.9	10	8	ADM78093	Adm78093 Human SJB
26	40	90.9	10	8	ADO16875	Ado16875 Murine an
27	40	90.9	10	8	ADO80122	Ado80122 Anti-huma
28	40	90.9	10	8	ADR15157	Adr15157 Mouse ant
29	40	90.9	10	8	ADP79386	Adp79386 Thyrotrop
30	40	90.9	10	9	ADV14598	Adv14598 CDR1 pept
31	40	90.9	10	9	ADY32279	Ady32279 Human Eph
32	40	90.9	10	9	ADZ08841	Adz08841 Mammalian
33	40	90.9	10	9	ADZ58528	Adz58528 VEGF rece
34	40	90.9	10	9	ADZ58525	Adz58525 VEGF rece
35	40	90.9	10	9	ADZ69235	Adz69235 IL-5R alp
36	40	90.9	10	9	ADZ52582	Adz52582 Mouse ant
37	40	90.9	10	9	ADZ48324	Adz48324 Pharmaceu
38	40	90.9	10	9	AEB17134	Aeb17134 EphA2-spe
39	40	90.9	10	9	AEA42934	Aea42934 EphA2 ant
40	40	90.9	10	9	AEA41148	Aea41148 Human leu
41	40	90.9	10	9	AEA99626	Aea99626 Human CAB
42	40	90.9	10	9	AEA99653	Aea99653 Human CAB
43	40	90.9	10	9	AEA99690	Aea99690 Human SW1
44	40	90.9	10	9	AEA99632	Aea99632 Human CAB
45	40	90.9	10	9	AED10376	Aed10376 Anti-myos
46	40	90.9	10	9	AED65196	Aed65196 Light cha
47	40	90.9	10	10	AEE70727	Aee70727 Mouse uPA
48	40	90.9	10	10	AEE98114	Aee98114 Murine PE
49	40	90.9	10	10	AEF51133	Aef51133 Variable
50	40	90.9	10	10	AEF76281	Aef76281 Prostate
51	39	88.6	10	3	AAY80143	Aay80143 Chimeric
52	39	88.6	10	4	AAO14425	Aao14425 CD25 bind
53	39	88.6	10	9	AED10374	Aed10374 Anti-myos
54	39	88.6	13	5	ADG67484	Adg67484 Humanised
55	39	88.6	13	5	ADG67413	Adg67413 Mouse ant
56	37	84.1	10	2	AAR27299	Aar27299 Consensus
57	37	84.1	10	2	AAW41382	Aaw41382 CDR1 of 1

SCORE Search Results Details for Application 10661366 and Search Result us-10-661-366-3.closed.ra1.

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OM protein - protein search, using sw model

Run on: August 9, 2006, 07:02:53 ; Search time 24.5902 Seconds
(without alignments)
35.596 Million cell updates/sec

Title: US-10-661-366-3
Perfect score: 44
Sequence: 1 SASSSVSYML 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 249102

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Database : Issued_Patents_AA:*
1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					
No.	Score	Match	Length	ID		Description

1	40	90.9	10	1	US-08-116-778E-9	Sequence 9, Appli
2	40	90.9	10	1	US-08-438-562-9	Sequence 9, Appli
3	40	90.9	10	1	US-08-483-528B-97	Sequence 97, Appl
4	40	90.9	10	2	US-08-836-561-49	Sequence 49, Appl
5	40	90.9	10	2	US-09-393-385B-108	Sequence 108, App
6	40	90.9	10	2	US-09-434-122-49	Sequence 49, Appl
7	40	90.9	10	2	US-09-563-222C-41	Sequence 41, Appl
8	40	90.9	10	2	US-09-798-689-4	Sequence 4, Appli
9	40	90.9	10	2	US-10-195-752-108	Sequence 108, App
10	40	90.9	10	2	US-09-453-718B-12	Sequence 12, Appl
11	40	90.9	10	2	US-09-453-718B-18	Sequence 18, Appl
12	39	88.6	10	2	US-08-479-089A-10	Sequence 10, Appl
13	39	88.6	10	2	US-07-669-545B-10	Sequence 10, Appl
14	37	84.1	10	1	US-07-946-421-1	Sequence 1, Appli
15	37	84.1	10	2	US-09-171-945-26	Sequence 26, Appl
16	37	84.1	10	2	US-09-910-059-26	Sequence 26, Appl
17	36	81.8	10	2	US-09-280-028-12	Sequence 12, Appl
18	36	81.8	10	2	US-09-091-071-3	Sequence 3, Appli
19	36	81.8	10	2	US-09-771-415-3	Sequence 3, Appli
20	36	81.8	10	2	US-09-996-288-14	Sequence 14, Appl
21	36	81.8	10	2	US-09-996-265-14	Sequence 14, Appl
22	36	81.8	11	1	US-08-432-694-2	Sequence 2, Appli
23	36	81.8	11	1	US-08-432-694-4	Sequence 4, Appli
24	33	75.0	10	2	US-08-783-853A-12	Sequence 12, Appl
25	33	75.0	10	2	US-09-344-050-12	Sequence 12, Appl
26	33	75.0	11	1	US-08-432-694-3	Sequence 3, Appli
27	33	75.0	12	1	US-08-482-228-42	Sequence 42, Appl
28	33	75.0	12	2	US-08-482-528-42	Sequence 42, Appl
29	33	75.0	14	1	US-08-482-228-46	Sequence 46, Appl
30	33	75.0	14	2	US-08-482-528-46	Sequence 46, Appl
31	32	72.7	10	2	US-09-996-288-144	Sequence 144, App
32	32	72.7	10	2	US-09-996-288-185	Sequence 185, App
33	32	72.7	10	2	US-09-996-288-191	Sequence 191, App
34	32	72.7	10	2	US-09-996-265-144	Sequence 144, App
35	32	72.7	10	2	US-09-996-265-185	Sequence 185, App
36	32	72.7	10	2	US-09-996-265-191	Sequence 191, App
37	32	72.7	11	1	US-08-432-694-8	Sequence 8, Appli
38	32	72.7	11	1	US-08-432-694-16	Sequence 16, Appl
39	31	70.5	10	2	US-09-996-288-39	Sequence 39, Appl
40	31	70.5	10	2	US-09-996-288-72	Sequence 72, Appl
41	31	70.5	10	2	US-09-996-288-122	Sequence 122, App
42	31	70.5	10	2	US-09-996-288-168	Sequence 168, App
43	31	70.5	10	2	US-09-996-265-39	Sequence 39, Appl
44	31	70.5	10	2	US-09-996-265-72	Sequence 72, Appl
45	31	70.5	10	2	US-09-996-265-122	Sequence 122, App
46	31	70.5	10	2	US-09-996-265-168	Sequence 168, App
47	31	70.5	11	1	US-08-432-694-10	Sequence 10, Appl
48	31	70.5	11	1	US-08-432-694-11	Sequence 11, Appl
49	31	70.5	11	1	US-08-432-694-12	Sequence 12, Appl
50	31	70.5	11	1	US-08-432-694-14	Sequence 14, Appl
51	31	70.5	11	1	US-08-432-694-15	Sequence 15, Appl
52	30	68.2	10	2	US-09-996-288-188	Sequence 188, App
53	30	68.2	10	2	US-09-996-265-188	Sequence 188, App
54	30	68.2	11	1	US-08-432-694-9	Sequence 9, Appli
55	29	65.9	10	1	US-08-432-694-5	Sequence 5, Appli
56	29	65.9	11	1	US-08-432-694-13	Sequence 13, Appl
57	28	63.6	10	2	US-09-996-288-104	Sequence 104, App
58	28	63.6	10	2	US-09-996-288-115	Sequence 115, App
59	28	63.6	10	2	US-09-996-288-129	Sequence 129, App
60	28	63.6	10	2	US-09-996-288-153	Sequence 153, App

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OM protein - protein search, using sw model

Run on: August 9, 2006, 07:35:38 ; Search time 79.5082 Seconds
(without alignments)
58.260 Million cell updates/sec

Title: US-10-661-366-3
Perfect score: 44
Sequence: 1 SASSSVSYML 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 395127

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Database : Published Applications_AA_Main:*
1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	44	100.0	10	5 US-10-661-366-3	Sequence 3, Appli

2	40	90.9	10	3	US-09-976-787-4	Sequence 4, Appli
3	40	90.9	10	3	US-09-865-198-4	Sequence 4, Appli
4	40	90.9	10	3	US-09-563-222-41	Sequence 41, Appl
5	40	90.9	10	3	US-09-798-689-4	Sequence 4, Appli
6	40	90.9	10	4	US-10-195-752-108	Sequence 108, App
7	40	90.9	10	4	US-10-160-232-12	Sequence 12, Appl
8	40	90.9	10	4	US-10-160-232-18	Sequence 18, Appl
9	40	90.9	10	4	US-10-283-349-49	Sequence 49, Appl
10	40	90.9	10	4	US-10-344-779-5	Sequence 5, Appli
11	40	90.9	10	4	US-10-436-782-2	Sequence 2, Appli
12	40	90.9	10	4	US-10-312-316-19	Sequence 19, Appl
13	40	90.9	10	4	US-10-738-809-5	Sequence 5, Appli
14	40	90.9	10	4	US-10-783-950-41	Sequence 41, Appl
15	40	90.9	10	5	US-10-482-630-4	Sequence 4, Appli
16	40	90.9	10	5	US-10-203-399B-4	Sequence 4, Appli
17	40	90.9	10	5	US-10-778-910-4	Sequence 4, Appli
18	40	90.9	10	5	US-10-810-881A-66	Sequence 66, Appl
19	40	90.9	10	5	US-10-809-387-4	Sequence 4, Appli
20	40	90.9	10	5	US-10-959-326-36	Sequence 36, Appl
21	40	90.9	10	6	US-11-004-795A-2	Sequence 2, Appli
22	40	90.9	10	6	US-11-004-794A-2	Sequence 2, Appli
23	40	90.9	10	6	US-11-193-512-49	Sequence 49, Appl
24	40	90.9	10	6	US-11-250-411-12	Sequence 12, Appl
25	40	90.9	10	6	US-11-250-411-18	Sequence 18, Appl
26	40	90.9	11	3	US-09-791-551-13	Sequence 13, Appl
27	39	88.6	10	3	US-09-770-002-4	Sequence 4, Appli
28	39	88.6	10	5	US-10-240-353B-4	Sequence 4, Appli
29	39	88.6	13	4	US-10-468-496-1905	Sequence 1905, Ap
30	39	88.6	13	4	US-10-468-496-1976	Sequence 1976, Ap
31	37	84.1	10	3	US-09-910-059-26	Sequence 26, Appl
32	37	84.1	10	4	US-10-232-187-8	Sequence 8, Appli
33	37	84.1	11	4	US-10-411-869A-38	Sequence 38, Appl
34	36	81.8	10	3	US-09-796-848A-5	Sequence 5, Appli
35	36	81.8	10	3	US-09-771-415-3	Sequence 3, Appli
36	36	81.8	10	3	US-09-996-288-14	Sequence 14, Appl
37	36	81.8	10	3	US-09-996-265-14	Sequence 14, Appl
38	36	81.8	10	4	US-10-020-354-14	Sequence 14, Appl
39	36	81.8	10	4	US-10-366-709-3	Sequence 3, Appli
40	36	81.8	10	4	US-10-461-863-14	Sequence 14, Appl
41	36	81.8	10	4	US-10-239-656-19	Sequence 19, Appl
42	36	81.8	10	4	US-10-657-363-3	Sequence 3, Appli
43	36	81.8	10	4	US-10-751-744-14	Sequence 14, Appl
44	36	81.8	10	5	US-10-900-230-14	Sequence 14, Appl
45	36	81.8	10	5	US-10-861-049-39	Sequence 39, Appl
46	36	81.8	10	5	US-10-962-285-14	Sequence 14, Appl
47	36	81.8	10	5	US-10-403-180-14	Sequence 14, Appl
48	36	81.8	10	6	US-11-021-874-39	Sequence 39, Appl
49	36	81.8	10	6	US-11-120-338-4	Sequence 4, Appli
50	36	81.8	10	6	US-11-106-820-4	Sequence 4, Appli
51	36	81.8	10	6	US-11-190-364-4	Sequence 4, Appli
52	36	81.8	10	6	US-11-147-780-4	Sequence 4, Appli
53	36	81.8	10	6	US-11-143-386-4	Sequence 4, Appli
54	35	79.5	10	5	US-10-994-091A-9	Sequence 9, Appli
55	34	77.3	10	6	US-11-009-939-8	Sequence 8, Appli
56	34	77.3	13	4	US-10-468-496-1904	Sequence 1904, Ap
57	34	77.3	13	4	US-10-468-496-1975	Sequence 1975, Ap
58	33	75.0	10	3	US-09-965-099-12	Sequence 12, Appl
59	33	75.0	10	4	US-10-051-852-12	Sequence 12, Appl
60	33	75.0	10	4	US-10-230-880-115	Sequence 115, App
61	33	75.0	10	4	US-10-430-176-12	Sequence 12, Appl
62	33	75.0	10	4	US-10-681-421-12	Sequence 12, Appl

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Page	List	Overview	FAQ	Suggestions

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OM protein - protein search, using sw model

Run on: August 9, 2006, 07:36:48 ; Search time 12.623 Seconds
(without alignments)
53.325 Million cell updates/sec

Title: US-10-661-366-3
Perfect score: 44
Sequence: 1 SASSSVSYML 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 239914 seqs, 67312017 residues

Total number of hits satisfying chosen parameters: 27373

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Database : Published_Applications_AA_New:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	%
Result	Query

No.	Score	Match	Length	DB	ID	Description
1	40	90.9	10	6	US-10-542-682-38	Sequence 38, Appl
2	36	81.8	10	6	US-10-513-148A-8	Sequence 8, Appli
3	36	81.8	10	7	US-11-254-182-57	Sequence 57, Appl
4	36	81.8	10	7	US-11-106-762-20	Sequence 20, Appl
5	36	81.8	10	7	US-11-263-230-14	Sequence 14, Appl
6	36	81.8	10	7	US-11-291-698A-44	Sequence 44, Appl
7	34	77.3	10	7	US-11-301-373-8	Sequence 8, Appli
8	32	72.7	10	7	US-11-263-230-144	Sequence 144, App
9	32	72.7	10	7	US-11-263-230-185	Sequence 185, App
10	32	72.7	10	7	US-11-263-230-191	Sequence 191, App
11	32	72.7	10	7	US-11-263-230-498	Sequence 498, App
12	31	70.5	10	7	US-11-254-182-67	Sequence 67, Appl
13	31	70.5	10	7	US-11-106-762-29	Sequence 29, Appl
14	31	70.5	10	7	US-11-238-281-35	Sequence 35, Appl
15	31	70.5	10	7	US-11-263-230-39	Sequence 39, Appl
16	31	70.5	10	7	US-11-263-230-72	Sequence 72, Appl
17	31	70.5	10	7	US-11-263-230-122	Sequence 122, App
18	31	70.5	10	7	US-11-263-230-168	Sequence 168, App
19	31	70.5	10	7	US-11-263-230-335	Sequence 335, App
20	31	70.5	12	7	US-11-376-338-12	Sequence 12, Appl
21	30	68.2	10	7	US-11-263-230-188	Sequence 188, App
22	30	68.2	10	7	US-11-263-230-452	Sequence 452, App
23	30	68.2	10	7	US-11-263-230-453	Sequence 453, App
24	28	63.6	10	6	US-10-542-682-37	Sequence 37, Appl
25	28	63.6	10	7	US-11-263-230-104	Sequence 104, App
26	28	63.6	10	7	US-11-263-230-115	Sequence 115, App
27	28	63.6	10	7	US-11-263-230-129	Sequence 129, App
28	28	63.6	10	7	US-11-263-230-153	Sequence 153, App
29	28	63.6	10	7	US-11-263-230-181	Sequence 181, App
30	28	63.6	10	7	US-11-263-230-193	Sequence 193, App
31	28	63.6	10	7	US-11-263-230-197	Sequence 197, App
32	28	63.6	10	7	US-11-263-230-489	Sequence 489, App
33	28	63.6	10	7	US-11-263-230-516	Sequence 516, App
34	27	61.4	10	6	US-10-542-682-55	Sequence 55, Appl
35	27	61.4	10	7	US-11-263-230-136	Sequence 136, App
36	27	61.4	10	7	US-11-263-230-146	Sequence 146, App
37	27	61.4	10	7	US-11-263-230-176	Sequence 176, App
38	27	61.4	10	7	US-11-263-230-183	Sequence 183, App
39	27	61.4	10	7	US-11-263-230-189	Sequence 189, App
40	27	61.4	10	7	US-11-263-230-499	Sequence 499, App
41	26	59.1	10	7	US-11-263-230-22	Sequence 22, Appl
42	26	59.1	10	7	US-11-263-230-31	Sequence 31, Appl
43	26	59.1	10	7	US-11-263-230-142	Sequence 142, App
44	26	59.1	10	7	US-11-263-230-186	Sequence 186, App
45	26	59.1	10	7	US-11-263-230-207	Sequence 207, App
46	26	59.1	10	7	US-11-263-230-412	Sequence 412, App
47	26	59.1	10	7	US-11-263-230-413	Sequence 413, App
48	26	59.1	10	7	US-11-263-230-442	Sequence 442, App
49	26	59.1	10	7	US-11-263-230-443	Sequence 443, App
50	26	59.1	10	7	US-11-263-230-447	Sequence 447, App
51	26	59.1	10	7	US-11-263-230-448	Sequence 448, App
52	26	59.1	10	7	US-11-263-230-495	Sequence 495, App
53	26	59.1	10	7	US-11-263-230-500	Sequence 500, App
54	26	59.1	10	7	US-11-263-230-501	Sequence 501, App
55	25	56.8	10	7	US-11-263-230-120	Sequence 120, App
56	25	56.8	10	7	US-11-263-230-169	Sequence 169, App
57	25	56.8	10	7	US-11-263-230-187	Sequence 187, App
58	25	56.8	10	7	US-11-263-230-454	Sequence 454, App
59	25	56.8	10	7	US-11-263-230-462	Sequence 462, App

SCORE Search

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OM protein - protein search, using sw model

Run on: August 9, 2006, 06:51:47 ; Search time 13.7705 Seconds
(without alignments)
69.872 Million cell updates/sec

Title: US-10-661-366-3
Perfect score: 44
Sequence: 1 SASSSVSYML 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 2523

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	22	50.0	11	2	PH0914	T-cell receptor be
2	22	50.0	15	2	B45115	peptidylprolyl iso
3	21	47.7	10	2	PH0948	T-cell receptor be
4	21	47.7	11	2	PH0941	T-cell receptor be
5	21	47.7	11	2	PH0924	T-cell receptor be
6	21	47.7	12	2	S47391	T-cell antigen rec
7	20	45.5	12	2	S47395	T-cell antigen rec
8	20	45.5	13	2	S47388	T-cell antigen rec

9	20	45.5	14	2	PH0774	T-cell receptor be
10	20	45.5	15	2	A38304	heterogeneous ribo
11	19	43.2	12	2	S26557	T-cell receptor be
12	19	43.2	13	2	S47362	T-cell antigen rec
13	19	43.2	13	2	PH1479	T-cell receptor be
14	18	40.9	8	2	PL0162	paramyosin - north
15	18	40.9	11	2	I60434	68kDa neurofilamen
16	18	40.9	13	2	S47359	T-cell antigen rec
17	18	40.9	14	2	I49514	B144 protein A - m
18	18	40.9	14	2	B61597	cytochrome P450 AL
19	17	38.6	9	2	PT0670	T-cell receptor be
20	17	38.6	13	2	S47377	T-cell antigen rec
21	17	38.6	13	2	S47384	T-cell antigen rec
22	17	38.6	14	2	PH1769	T cell receptor al
23	17	38.6	14	2	PH1601	Ig H chain V-D-J r
24	17	38.6	14	2	C48394	major fat-globule
25	17	38.6	15	2	A27504	histone H2A - mous
26	17	38.6	15	2	A35417	28K serine protein
27	16	36.4	6	2	PT0593	T-cell receptor be
28	16	36.4	7	2	PT0620	T-cell receptor be
29	16	36.4	8	2	S68802	nitrate reductase
30	16	36.4	10	2	PH0927	T-cell receptor be
31	16	36.4	11	2	PT0211	T-cell receptor al
32	16	36.4	11	2	PH0903	T-cell receptor be
33	16	36.4	11	2	PH0922	T-cell receptor be
34	16	36.4	12	2	PH0746	T-cell receptor be
35	16	36.4	12	2	PH1470	T-cell receptor be
36	16	36.4	14	2	S22236	lipxygenase (EC 1
37	16	36.4	14	2	PH0765	T-cell receptor be
38	16	36.4	15	2	S51735	T-cell receptor be
39	16	36.4	15	2	A49887	transcription fact
40	16	36.4	15	2	B45133	casein kinase II (
41	15	34.1	7	2	S09027	carboxylesterase (
42	15	34.1	10	2	PH0944	T-cell receptor be
43	15	34.1	10	2	PH0895	T-cell receptor be
44	15	34.1	12	2	S47394	T-cell antigen rec
45	15	34.1	12	2	PH0771	T-cell receptor be
46	15	34.1	12	2	F84132	hypothetical prote
47	15	34.1	13	2	PN0176	acidic ribosomal p
48	15	34.1	13	2	S47392	T-cell antigen rec
49	15	34.1	14	2	A60770	cell surface alloa
50	15	34.1	15	2	B56661	S-locus specific g
51	15	34.1	15	2	S32677	nitrogenase cofact
52	15	34.1	15	2	A40634	orf19 3' of eryK -
53	15	34.1	15	2	A31435	adherence lectin h
54	14	31.8	10	2	S28055	cytochrome b559 co
55	14	31.8	11	2	PH0891	T-cell receptor be
56	14	31.8	12	2	PH1324	Ig heavy chain DJ
57	14	31.8	12	2	S47393	T-cell antigen rec
58	14	31.8	12	2	S51737	T-cell receptor be
59	14	31.8	12	2	PH0802	T-cell receptor al
60	14	31.8	13	2	S09395	hypothetical prote
61	14	31.8	13	2	S47356	T-cell antigen rec
62	14	31.8	13	2	S47381	T-cell antigen rec
63	14	31.8	13	2	S47385	T-cell antigen rec
64	14	31.8	13	2	S47400	T-cell antigen rec
65	14	31.8	13	2	PH0928	T-cell receptor be
66	14	31.8	14	2	S29209	avenin alpha-2 - o
67	14	31.8	14	2	E33098	214K exoantigen (v
68	14	31.8	14	2	B20872	alpha-2-macroglobu
69	14	31.8	14	2	F83754	hypothetical prote

SCORE Search Results Details for Application 10661366 and Search Result us-10-661-366-3.closed.rup.

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OM protein - protein search, using sw model

Run on: August 9, 2006, 06:40:52 ; Search time 111.475 Seconds
(without alignments)
82.979 Million cell updates/sec

Title: US-10-661-366-3
Perfect score: 44
Sequence: 1 SASSSVSYML 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 8966

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Database : UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	22	50.0	14	2	Q4JHP1_9CARY	Q4jhp1 suaeda liao
2	20	45.5	15	2	Q41209_SOLTU	Q41209 solanum tub
3	19	43.2	9	2	Q96T78_HUMAN	Q96t78 homo sapien
4	19	43.2	9	2	Q9PS68_CHICK	Q9ps68 gallus gall

5	19	43.2	13	1	PROFX_ORYSA	P83647	oryza sativ
6	18	40.9	8	2	Q7M4A4_MERMC	Q7m4a4	mercenaria
7	18	40.9	8	2	Q83332_9CORO	Q83332	murine hepa
8	18	40.9	9	2	Q69349_HHV2	Q69349	human herpe
9	18	40.9	10	1	FAR2_PENMO	P83317	penaeus mon
10	18	40.9	10	2	Q8GUV6_9BRAS	Q8guv6	capsella ru
11	18	40.9	10	2	Q6YBH6_STRPN	Q6ybh6	streptococc
12	18	40.9	12	2	Q9SQF8_PINTA	Q9sqf8	pinus taeda
13	18	40.9	14	2	Q7M047_RAT	Q7m047	rattus norv
14	18	40.9	14	2	Q9Z1H4_MOUSE	Q9z1h4	mus musculu
15	18	40.9	15	2	Q6ZZ63_9CARY	Q6zz63	silene nigr
16	17	38.6	9	2	Q2XN93_LYCES	Q2xn93	lycopersico
17	17	38.6	10	2	Q7WUG2_ECOLI	Q7wug2	escherichia
18	17	38.6	11	2	Q5TLA1_CLAPU	Q5tla1	claviceps p
19	17	38.6	11	2	Q6SE50_DROSI	Q6se50	drosophila
20	17	38.6	11	2	Q8RMI8_ENTHR	Q8rmi8	enterococcu
21	17	38.6	11	2	Q6E5N1_9SAUR	Q6e5n1	ptyctolaemu
22	17	38.6	11	2	Q9G607_9SAUR	Q9g607	aphaniotis
23	17	38.6	12	1	PVK21_CELBM	P84374	celatoblatt
24	17	38.6	12	2	Q6EEI9_PIG	Q6eei9	sus scrofa
25	17	38.6	12	2	Q83139_BSMV	Q83139	barley stri
26	17	38.6	13	2	Q7BS48_STRAU	Q7bs48	streptomyce
27	17	38.6	13	2	Q7TMB4_MOUSE	Q7tmb4	mus musculu
28	17	38.6	14	2	Q6LCK3_HUMAN	Q6lck3	homo sapien
29	17	38.6	14	2	Q8IVK4_HUMAN	Q8ivk4	homo sapien
30	17	38.6	14	2	Q9NFK8_BRUPA	Q9nfk8	brugia paha
31	17	38.6	14	2	Q4L9K3_STAHJ	Q4l9k3	staphylococ
32	17	38.6	15	2	Q7RHM0_PLAYO	Q7rhm0	plasmodium
33	17	38.6	15	2	Q7M3G3_BOVIN	Q7m3g3	bos taurus
34	17	38.6	15	2	Q5SBT4_9POAL	Q5sbt4	thamnochort
35	17	38.6	15	2	Q5SBV0_9POAL	Q5sbv0	thamnochort
36	16	36.4	8	2	Q8WGC9_9EUCA	Q8wgc9	upogebia af
37	16	36.4	9	1	FLAA2_TREHY	P80159	treponema h
38	16	36.4	9	2	Q28112_BOVIN	Q28112	bos taurus
39	16	36.4	10	2	Q67B22_9CAUD	Q67b22	bacterioph
40	16	36.4	11	2	Q9HFN8_CANRU	Q9hfn8	candida rug
41	16	36.4	12	2	Q683W7_HUMAN	Q683w7	homo sapien
42	16	36.4	12	2	Q4X448_PLACH	Q4x448	plasmodium
43	16	36.4	12	2	Q50959_NEIGO	Q50959	neisseria g
44	16	36.4	12	2	Q84AV9_9ENTR	Q84av9	buchnera ap
45	16	36.4	12	2	Q5IT10_9CALI	Q5it10	norovirus c
46	16	36.4	13	1	RAN6_RANCA	P82821	rana catesb
47	16	36.4	13	1	RAN7_RANCA	P82822	rana catesb
48	16	36.4	13	1	UN41_CLOPA	P81360	clostridium
49	16	36.4	13	2	Q29823_HUMAN	Q29823	homo sapien
50	16	36.4	13	2	Q6PJ24_HUMAN	Q6pj24	homo sapien
51	16	36.4	13	2	Q9TWM3_LOCFI	Q9twm3	locusta mig
52	16	36.4	14	1	ADFA_TENMO	P82965	tenebrio mo
53	16	36.4	14	2	Q9MRF6_9POAL	Q9mrf6	hordeum mur
54	16	36.4	14	2	Q67112_9INFA	Q67112	influenza a
55	16	36.4	14	2	Q84708_9CORO	Q84708	porcine epi
56	16	36.4	15	2	Q7RU13_NEUCR	Q7ru13	neurospora
57	16	36.4	15	2	Q9UCM0_HUMAN	Q9ucm0	homo sapien
58	16	36.4	15	2	Q4YF12_PLABE	Q4yf12	plasmodium
59	16	36.4	15	2	Q7RHB9_PLAYO	Q7rhb9	plasmodium
60	16	36.4	15	2	Q9TRL0_CANFA	Q9trl0	canis famil
61	16	36.4	15	2	Q97092_9HIV1	Q97092	human immun
62	15	34.1	9	2	Q9BYF9_HUMAN	Q9byf9	homo sapien
63	15	34.1	9	2	P82208_BOMMO	P82208	bombyx mori
64	15	34.1	9	2	Q8HZY2_CANFA	Q8hzy2	canis famil
65	15	34.1	9	2	Q9K4M6_STAHA	Q9k4m6	staphylococ

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OM protein - protein search, using sw model

Run on: August 9, 2006, 07:45:18 ; Search time 25.256 Seconds
(without alignments)
181.033 Million cell updates/sec

Title: US-10-661-366-3
Perfect score: 44
Sequence: 1 SASSSVSYML 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : A_Geneseq_8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	44	100.0	10	9	ADY75168	Ady75168 Antibody
2	44	100.0	106	5	AAE27838	Aae27838 Mouse KS
3	44	100.0	106	5	AAE27827	Aae27827 Mouse KS
4	44	100.0	106	5	AAE27831	Aae27831 Mouse KS
5	44	100.0	106	5	AAE27833	Aae27833 Mouse KS
6	44	100.0	106	5	AAE27835	Aae27835 Mouse KS
7	44	100.0	106	5	AAE27836	Aae27836 Mouse KS
8	44	100.0	106	5	AAE27840	Aae27840 Mouse KS
9	44	100.0	106	5	ADG67536	Adg67536 KS antibo
10	44	100.0	106	5	ADG67544	Adg67544 KS antibo
11	44	100.0	106	5	ADG67538	Adg67538 KS antibo
12	44	100.0	106	5	ADG67530	Adg67530 KS antibo
13	44	100.0	106	5	ADG67534	Adg67534 KS antibo
14	44	100.0	106	5	ADG67542	Adg67542 KS antibo
15	44	100.0	106	5	ADG67540	Adg67540 KS antibo
16	44	100.0	106	6	AAE33427	Aae33427 Murine KS
17	44	100.0	106	6	AAE33426	Aae33426 KS-1/4 an
18	44	100.0	106	6	AAE33425	Aae33425 Murine KS
19	44	100.0	106	6	AAE33428	Aae33428 Murine KS
20	44	100.0	106	6	AAE33419	Aae33419 Murine KS
21	44	100.0	106	6	AAE33422	Aae33422 Murine KS
22	44	100.0	106	6	AAE33424	Aae33424 Murine KS
23	44	100.0	106	6	AAE33420	Aae33420 Murine KS
24	44	100.0	106	6	AAE33421	Aae33421 Murine KS
25	44	100.0	106	6	AAE33413	Aae33413 Murine KS
26	44	100.0	106	6	AAO30909	Aao30909 hu-KS ant
27	44	100.0	107	1	AAP93039	Aap93039 Recombina
28	44	100.0	107	1	AAP93040	Aap93040 Recombina
29	44	100.0	107	9	ADY75167	Ady75167 Antibody
30	44	100.0	213	1	AAP93035	Aap93035 Chimeric
31	44	100.0	213	6	AAE33445	Aae33445 KS antibo
32	40	90.9	10	2	AAW27424	Aaw27424 CDR1 from
33	40	90.9	10	2	AAW73169	Aaw73169 CDR1 of 1
34	40	90.9	10	2	AAZ28390	Aay28390 Peptide f
35	40	90.9	10	3	AAZ77582	Aay77582 Anti-huma
36	40	90.9	10	3	AAZ77588	Aay77588 Anti-huma
37	40	90.9	10	3	AAZ97232	Aay97232 Complemen
38	40	90.9	10	4	AAB82706	Aab82706 VEGF anta
39	40	90.9	10	4	AAE13140	Aae13140 Humanised
40	40	90.9	10	4	AAB83163	Aab83163 Mouse gan
41	40	90.9	10	4	AAB78857	Aab78857 Anti-huma
42	40	90.9	10	4	AAB78851	Aab78851 Anti-huma
43	40	90.9	10	5	AAU81247	Aau81247 Murine tr
44	40	90.9	10	5	AAE25952	Aae25952 Mouse ant
45	40	90.9	10	5	AAU74409	Aau74409 Light cha
46	40	90.9	10	5	AAU70361	Aau70361 Mouse Kap
47	40	90.9	10	5	ABB75618	Abb75618 Anti-RANK
48	40	90.9	10	6	ABJ26721	Abj26721 VEGF bind
49	40	90.9	10	8	ADE85698	Ade85698 Human Eph
50	40	90.9	10	8	ADH77348	Adh77348 Yeast kil
51	40	90.9	10	8	ADH77354	Adh77354 Yeast kil
52	40	90.9	10	8	ADL11883	Adl11883 CDR-1 lig
53	40	90.9	10	8	ADL11880	Adl11880 CDR-1 lig
54	40	90.9	10	8	ADK18198	Adk18198 Mouse VEG
55	40	90.9	10	8	ADM78093	Adm78093 Human SJB
56	40	90.9	10	8	ADO16875	Ado16875 Murine an
57	40	90.9	10	8	ADO80122	Ado80122 Anti-huma

1	44	100.0	106	2	US-10-138-727A-1	Sequence 1, Appli
2	44	100.0	106	2	US-10-138-727A-7	Sequence 7, Appli
3	44	100.0	106	2	US-10-138-727A-8	Sequence 8, Appli
4	44	100.0	106	2	US-10-138-727A-9	Sequence 9, Appli
5	44	100.0	106	2	US-10-138-727A-10	Sequence 10, Appl
6	44	100.0	106	2	US-10-138-727A-12	Sequence 12, Appl
7	44	100.0	106	2	US-10-138-727A-13	Sequence 13, Appl
8	44	100.0	106	2	US-10-138-727A-14	Sequence 14, Appl
9	44	100.0	106	2	US-10-138-727A-15	Sequence 15, Appl
10	44	100.0	106	2	US-10-138-727A-16	Sequence 16, Appl
11	44	100.0	213	2	US-10-138-727A-42	Sequence 42, Appl
12	40	90.9	10	1	US-08-116-778E-9	Sequence 9, Appli
13	40	90.9	10	1	US-08-438-562-9	Sequence 9, Appli
14	40	90.9	10	1	US-08-483-528B-97	Sequence 97, Appl
15	40	90.9	10	2	US-08-836-561-49	Sequence 49, Appl
16	40	90.9	10	2	US-09-393-385B-108	Sequence 108, App
17	40	90.9	10	2	US-09-434-122-49	Sequence 49, Appl
18	40	90.9	10	2	US-09-563-222C-41	Sequence 41, Appl
19	40	90.9	10	2	US-09-798-689-4	Sequence 4, Appli
20	40	90.9	10	2	US-10-195-752-108	Sequence 108, App
21	40	90.9	10	2	US-09-453-718B-12	Sequence 12, Appl
22	40	90.9	10	2	US-09-453-718B-18	Sequence 18, Appl
23	40	90.9	97	2	US-09-280-028-4	Sequence 4, Appli
24	40	90.9	100	1	US-08-308-494A-19	Sequence 19, Appl
25	40	90.9	104	2	US-09-453-718B-100	Sequence 100, App
26	40	90.9	104	2	US-09-453-718B-104	Sequence 104, App
27	40	90.9	104	2	US-09-453-718B-105	Sequence 105, App
28	40	90.9	104	2	US-09-453-718B-107	Sequence 107, App
29	40	90.9	105	2	US-08-434-000A-12	Sequence 12, Appl
30	40	90.9	105	2	US-09-312-157-12	Sequence 12, Appl
31	40	90.9	105	2	US-09-717-888-12	Sequence 12, Appl
32	40	90.9	105	2	US-09-453-718B-108	Sequence 108, App
33	40	90.9	105	2	US-09-453-718B-109	Sequence 109, App
34	40	90.9	105	2	US-09-453-718B-110	Sequence 110, App
35	40	90.9	105	2	US-09-453-718B-111	Sequence 111, App
36	40	90.9	106	2	US-08-397-411-8	Sequence 8, Appli
37	40	90.9	106	2	US-08-397-411-9	Sequence 9, Appli
38	40	90.9	106	2	US-09-798-689-8	Sequence 8, Appli
39	40	90.9	106	2	US-10-138-727A-11	Sequence 11, Appl
40	40	90.9	106	2	US-09-453-718B-98	Sequence 98, Appl
41	40	90.9	106	2	US-09-453-718B-103	Sequence 103, App
42	40	90.9	107	1	US-08-303-569B-25	Sequence 25, Appl
43	40	90.9	107	1	US-08-303-569B-26	Sequence 26, Appl
44	40	90.9	107	1	US-08-303-569B-27	Sequence 27, Appl
45	40	90.9	107	1	US-08-303-569B-28	Sequence 28, Appl
46	40	90.9	107	1	US-08-303-569B-29	Sequence 29, Appl
47	40	90.9	107	1	US-08-070-116A-6	Sequence 6, Appli
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50	40	90.9	107	1	US-08-070-116A-18	Sequence 18, Appl
51	40	90.9	107	1	US-08-116-247-8	Sequence 8, Appli
52	40	90.9	107	1	US-08-116-247-26	Sequence 26, Appl
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54	40	90.9	107	1	US-08-116-247-28	Sequence 28, Appl
55	40	90.9	107	1	US-08-116-247-29	Sequence 29, Appl
56	40	90.9	107	2	US-08-557-050-6	Sequence 6, Appli
57	40	90.9	107	2	US-08-557-050-8	Sequence 8, Appli
58	40	90.9	107	2	US-08-557-050-9	Sequence 9, Appli
59	40	90.9	107	2	US-09-795-515-25	Sequence 25, Appl
60	40	90.9	107	2	US-09-795-515-26	Sequence 26, Appl

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OM protein - protein search, using sw model

Run on: August 9, 2006, 09:01:05 ; Search time 21.3993 Seconds
(without alignments)
216.462 Million cell updates/sec

Title: US-10-661-366-3
Perfect score: 44
Sequence: 1 SASSSVSYML 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Published_Applications_AA_Main:*

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- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Match	Query	Length	DB	ID	Description
No.							

1	44	100.0	10	5	US-10-661-366-3	Sequence 3, Appli
2	44	100.0	106	4	US-10-138-727A-1	Sequence 1, Appli
3	44	100.0	106	4	US-10-138-727A-7	Sequence 7, Appli
4	44	100.0	106	4	US-10-138-727A-8	Sequence 8, Appli
5	44	100.0	106	4	US-10-138-727A-9	Sequence 9, Appli
6	44	100.0	106	4	US-10-138-727A-10	Sequence 10, Appl
7	44	100.0	106	4	US-10-138-727A-12	Sequence 12, Appl
8	44	100.0	106	4	US-10-138-727A-13	Sequence 13, Appl
9	44	100.0	106	4	US-10-138-727A-14	Sequence 14, Appl
10	44	100.0	106	4	US-10-138-727A-15	Sequence 15, Appl
11	44	100.0	106	4	US-10-138-727A-16	Sequence 16, Appl
12	44	100.0	106	4	US-10-310-719-31	Sequence 31, Appl
13	44	100.0	106	4	US-10-468-370-659	Sequence 659, App
14	44	100.0	106	4	US-10-468-370-663	Sequence 663, App
15	44	100.0	106	4	US-10-468-370-665	Sequence 665, App
16	44	100.0	106	4	US-10-468-370-667	Sequence 667, App
17	44	100.0	106	4	US-10-468-370-669	Sequence 669, App
18	44	100.0	106	4	US-10-468-370-671	Sequence 671, App
19	44	100.0	106	4	US-10-468-370-673	Sequence 673, App
20	44	100.0	106	4	US-10-468-496-2022	Sequence 2022, Ap
21	44	100.0	106	4	US-10-468-496-2026	Sequence 2026, Ap
22	44	100.0	106	4	US-10-468-496-2028	Sequence 2028, Ap
23	44	100.0	106	4	US-10-468-496-2030	Sequence 2030, Ap
24	44	100.0	106	4	US-10-468-496-2032	Sequence 2032, Ap
25	44	100.0	106	4	US-10-468-496-2034	Sequence 2034, Ap
26	44	100.0	106	4	US-10-468-496-2036	Sequence 2036, Ap
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28	44	100.0	106	6	US-11-174-186-7	Sequence 7, Appli
29	44	100.0	106	6	US-11-174-186-8	Sequence 8, Appli
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31	44	100.0	106	6	US-11-174-186-10	Sequence 10, Appl
32	44	100.0	106	6	US-11-174-186-12	Sequence 12, Appl
33	44	100.0	106	6	US-11-174-186-13	Sequence 13, Appl
34	44	100.0	106	6	US-11-174-186-14	Sequence 14, Appl
35	44	100.0	106	6	US-11-174-186-15	Sequence 15, Appl
36	44	100.0	106	6	US-11-174-186-16	Sequence 16, Appl
37	44	100.0	107	5	US-10-661-366-2	Sequence 2, Appli
38	44	100.0	213	4	US-10-138-727A-42	Sequence 42, Appl
39	44	100.0	213	6	US-11-174-186-42	Sequence 42, Appl
40	40	90.9	10	3	US-09-976-787-4	Sequence 4, Appli
41	40	90.9	10	3	US-09-865-198-4	Sequence 4, Appli
42	40	90.9	10	3	US-09-563-222-41	Sequence 41, Appl
43	40	90.9	10	3	US-09-798-689-4	Sequence 4, Appli
44	40	90.9	10	4	US-10-195-752-108	Sequence 108, App
45	40	90.9	10	4	US-10-160-232-12	Sequence 12, Appl
46	40	90.9	10	4	US-10-160-232-18	Sequence 18, Appl
47	40	90.9	10	4	US-10-283-349-49	Sequence 49, Appl
48	40	90.9	10	4	US-10-344-779-5	Sequence 5, Appli
49	40	90.9	10	4	US-10-436-782-2	Sequence 2, Appli
50	40	90.9	10	4	US-10-312-316-19	Sequence 19, Appl
51	40	90.9	10	4	US-10-738-809-5	Sequence 5, Appli
52	40	90.9	10	4	US-10-783-950-41	Sequence 41, Appl
53	40	90.9	10	5	US-10-482-630-4	Sequence 4, Appli
54	40	90.9	10	5	US-10-203-399B-4	Sequence 4, Appli
55	40	90.9	10	5	US-10-778-910-4	Sequence 4, Appli
56	40	90.9	10	5	US-10-810-881A-66	Sequence 66, Appl
57	40	90.9	10	5	US-10-809-387-4	Sequence 4, Appli
58	40	90.9	10	5	US-10-959-326-36	Sequence 36, Appl
59	40	90.9	10	6	US-11-004-795A-2	Sequence 2, Appli
60	40	90.9	10	6	US-11-004-794A-2	Sequence 2, Appli
61	40	90.9	10	6	US-11-193-512-49	Sequence 49, Appl

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OM protein - protein search, using sw model

Run on: August 9, 2006, 09:02:15 ; Search time 3.27645 Seconds
(without alignments)
205.442 Million cell updates/sec

Title: US-10-661-366-3
Perfect score: 44
Sequence: 1 SASSSVSYML 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 239914 seqs, 67312017 residues

Total number of hits satisfying chosen parameters: 239914

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Published_Applications_AA_New:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	% Query
--------	------------

No.	Score	Match	Length	DB	ID	Description
1	40	90.9	10	6	US-10-542-682-38	Sequence 38, Appl
2	40	90.9	106	6	US-10-542-682-18	Sequence 18, Appl
3	40	90.9	110	6	US-10-514-516-6	Sequence 6, Appli
4	40	90.9	128	6	US-10-528-928-10	Sequence 10, Appl
5	40	90.9	242	7	US-11-183-325-20	Sequence 20, Appl
6	40	90.9	605	6	US-10-514-516-2	Sequence 2, Appli
7	36	81.8	10	6	US-10-513-148A-8	Sequence 8, Appli
8	36	81.8	10	7	US-11-254-182-57	Sequence 57, Appl
9	36	81.8	10	7	US-11-106-762-20	Sequence 20, Appl
10	36	81.8	10	7	US-11-263-230-14	Sequence 14, Appl
11	36	81.8	10	7	US-11-291-698A-44	Sequence 44, Appl
12	36	81.8	26	7	US-11-238-281-4	Sequence 4, Appli
13	36	81.8	26	7	US-11-238-281-5	Sequence 5, Appli
14	36	81.8	106	7	US-11-263-230-13	Sequence 13, Appl
15	36	81.8	106	7	US-11-263-230-54	Sequence 54, Appl
16	36	81.8	106	7	US-11-263-230-56	Sequence 56, Appl
17	36	81.8	106	7	US-11-263-230-58	Sequence 58, Appl
18	36	81.8	106	7	US-11-263-230-60	Sequence 60, Appl
19	36	81.8	106	7	US-11-263-230-62	Sequence 62, Appl
20	36	81.8	106	7	US-11-263-230-65	Sequence 65, Appl
21	36	81.8	106	7	US-11-263-230-70	Sequence 70, Appl
22	36	81.8	106	7	US-11-263-230-307	Sequence 307, App
23	36	81.8	106	7	US-11-256-060-3	Sequence 3, Appli
24	36	81.8	107	6	US-10-513-148A-16	Sequence 16, Appl
25	36	81.8	107	7	US-11-254-182-25	Sequence 25, Appl
26	36	81.8	107	7	US-11-254-182-26	Sequence 26, Appl
27	36	81.8	107	7	US-11-106-762-1	Sequence 1, Appli
28	36	81.8	107	7	US-11-106-762-17	Sequence 17, Appl
29	36	81.8	107	7	US-11-106-762-18	Sequence 18, Appl
30	36	81.8	107	7	US-11-238-281-1	Sequence 1, Appli
31	36	81.8	107	7	US-11-238-281-2	Sequence 2, Appli
32	36	81.8	107	7	US-11-291-698A-41	Sequence 41, Appl
33	36	81.8	107	7	US-11-291-698A-42	Sequence 42, Appl
34	36	81.8	129	6	US-10-513-148A-4	Sequence 4, Appli
35	36	81.8	213	7	US-11-254-182-63	Sequence 63, Appl
36	36	81.8	213	7	US-11-106-762-3	Sequence 3, Appli
37	36	81.8	213	7	US-11-106-762-24	Sequence 24, Appl
38	36	81.8	213	7	US-11-238-281-13	Sequence 13, Appl
39	36	81.8	213	7	US-11-263-230-211	Sequence 211, App
40	36	81.8	213	7	US-11-263-230-231	Sequence 231, App
41	36	81.8	213	7	US-11-263-230-233	Sequence 233, App
42	36	81.8	213	7	US-11-263-230-235	Sequence 235, App
43	36	81.8	213	7	US-11-263-230-237	Sequence 237, App
44	36	81.8	213	7	US-11-263-230-239	Sequence 239, App
45	36	81.8	213	7	US-11-263-230-241	Sequence 241, App
46	36	81.8	213	7	US-11-263-230-243	Sequence 243, App
47	36	81.8	213	7	US-11-263-230-247	Sequence 247, App
48	36	81.8	213	7	US-11-263-230-306	Sequence 306, App
49	36	81.8	232	7	US-11-106-762-23	Sequence 23, Appl
50	36	81.8	232	7	US-11-291-698A-56	Sequence 56, Appl
51	36	81.8	242	7	US-11-183-325-18	Sequence 18, Appl
52	35	79.5	118	6	US-10-513-539A-4	Sequence 4, Appli
53	35	79.5	118	6	US-10-513-539A-8	Sequence 8, Appli
54	35	79.5	128	7	US-11-315-067-4	Sequence 4, Appli
55	35	79.5	128	7	US-11-315-067-6	Sequence 6, Appli
56	34	77.3	10	7	US-11-301-373-8	Sequence 8, Appli
57	34	77.3	106	7	US-11-301-373-46	Sequence 46, Appl
58	34	77.3	107	7	US-11-301-373-7	Sequence 7, Appli
59	34	77.3	217	6	US-10-953-349-28671	Sequence 28671, A

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This page gives you Search Results detail for the Application 10661366 and Search Result us-10-661-3... [start](#)

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OM protein - protein search, using sw model

Run on: August 9, 2006, 08:00:49 ; Search time 3.92491 Seconds
(without alignments)
245.144 Million cell updates/sec

Title: US-10-661-366-3
Perfect score: 44
Sequence: 1 SASSSVSYML 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : PIR_80:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	40	90.9	90	2 S26339	Ig kappa chain V r
2	40	90.9	91	2 S17627	Ig kappa chain V r
3	40	90.9	91	2 S17629	Ig kappa chain V r
4	40	90.9	91	2 S17639	Ig kappa chain V r
5	40	90.9	91	2 S17637	Ig kappa chain V r
6	40	90.9	94	2 S20653	Ig heavy chain V r
7	40	90.9	94	2 S20650	Ig heavy chain V r
8	40	90.9	94	2 S26340	Ig light chain V r

9	40	90.9	97	2	S26341	Ig light chain V r
10	40	90.9	97	2	PH1084	Ig light chain V r
11	40	90.9	97	2	PH1085	Ig light chain V r
12	40	90.9	99	2	S29585	Ig kappa chain V r
13	40	90.9	99	2	D38601	Ig kappa chain V r
14	40	90.9	100	2	S29590	Ig kappa chain V r
15	40	90.9	102	2	S24214	Ig kappa chain - m
16	40	90.9	102	2	S11115	Ig kappa chain V r
17	40	90.9	103	2	S29591	Ig kappa chain V r
18	40	90.9	104	2	B49049	Ig kappa chain V r
19	40	90.9	105	2	S26338	Ig kappa chain V r
20	40	90.9	106	2	PS0071	Ig kappa chain V r
21	40	90.9	106	2	S11114	Ig kappa chain V r
22	40	90.9	106	2	PS0070	Ig kappa chain V r
23	40	90.9	106	2	B54378	Ig light chain V r
24	40	90.9	106	2	PS0072	Ig kappa chain V r
25	40	90.9	106	2	S11120	Ig kappa chain V r
26	40	90.9	107	1	KVMSX4	Ig kappa chain V r
27	40	90.9	107	2	S11112	Ig kappa chain V r
28	40	90.9	107	2	S11118	Ig kappa chain V r
29	40	90.9	107	2	S11116	Ig kappa chain V r
30	40	90.9	107	2	S11113	Ig kappa chain V r
31	40	90.9	107	2	PT0401	Ig light chain V r
32	40	90.9	107	2	PT0400	Ig light chain V r
33	40	90.9	107	2	PT0395	Ig light chain V r
34	40	90.9	107	2	PT0402	Ig light chain V r
35	40	90.9	107	2	S11119	Ig kappa chain V r
36	40	90.9	107	2	S11123	Ig kappa chain V r
37	40	90.9	107	2	PT0403	Ig light chain V r
38	40	90.9	107	2	PT0398	Ig light chain V r
39	40	90.9	107	2	S11121	Ig kappa chain V r
40	40	90.9	107	2	S11117	Ig kappa chain V r
41	40	90.9	107	2	PT0399	Ig light chain V r
42	40	90.9	107	2	A30562	Ig kappa chain V r
43	40	90.9	107	2	S11122	Ig kappa chain V r
44	40	90.9	107	2	PT0406	Ig kappa chain V r
45	40	90.9	107	2	B30562	Ig kappa chain V r
46	40	90.9	108	2	S11125	Ig kappa chain V r
47	40	90.9	108	2	G30560	Ig kappa chain V r
48	40	90.9	108	2	S38720	Ig light chain V r
49	40	90.9	130	1	JL0079	Ig kappa chain pre
50	40	90.9	132	2	S05268	Ig kappa chain pre
51	40	90.9	140	2	PL0013	Ig kappa chain pre
52	39	88.6	107	2	PD0011	Ig kappa chain V r
53	39	88.6	107	2	PC4405	Ig kappa chain V r
54	37	84.1	76	2	A48784	Ig kappa V regions
55	37	84.1	91	2	S17626	Ig kappa chain V r
56	36	81.8	91	2	S17630	Ig kappa chain V r
57	36	81.8	91	2	S17628	Ig kappa chain V r
58	36	81.8	104	2	JC6076	anti-D-dimer monoc
59	36	81.8	106	2	PL0082	Ig kappa chain V r
60	35	79.5	95	2	D33730	Ig kappa chain V r
61	35	79.5	106	2	G27887	Ig kappa chain V r
62	35	79.5	107	2	PT0396	Ig light chain V r
63	35	79.5	175	2	G72683	hypothetical prote
64	34	77.3	377	2	C64404	hypothetical prote
65	34	77.3	420	2	AG0958	probable membrane
66	34	77.3	1788	2	T31095	vitellogenin precu
67	34	77.3	1800	2	AI1918	serine/threonine k
68	33	75.0	619	2	AH2244	two-component sens
69	33	75.0	669	2	E84852	hypothetical prote

SCORE Search Results Details for Application 10661366 and Search Result us-10-661-366-3.rup.

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OM protein - protein search, using sw model

Run on: August 9, 2006, 07:46:18 ; Search time 30.2389 Seconds
(without alignments)
305.902 Million cell updates/sec

Title: US-10-661-366-3
Perfect score: 44
Sequence: 1 SASSSVSYML 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	40	90.9	107	1 KV6A_MOUSE	P01675 mus musculu
2	40	90.9	107	1 KV6B_MOUSE	P01676 mus musculu
3	40	90.9	107	1 KV6C_MOUSE	P01677 mus musculu
4	40	90.9	107	1 KV6D_MOUSE	P01678 mus musculu

5	40	90.9	107	1	KV6F_MOUSE	P04940	mus musculu
6	40	90.9	107	1	KV6G_MOUSE	P04941	mus musculu
7	40	90.9	107	1	KV6H_MOUSE	P04942	mus musculu
8	40	90.9	107	1	KV6I_MOUSE	P04943	mus musculu
9	40	90.9	107	1	KV6J_MOUSE	P04944	mus musculu
10	40	90.9	108	1	KV6K_MOUSE	P04945	mus musculu
11	40	90.9	112	2	Q8K1F0_MOUSE	Q8klf0	mus musculu
12	40	90.9	112	2	Q8K1F3_MOUSE	Q8klf3	mus musculu
13	39	88.6	134	2	Q8VDD0_MOUSE	Q8vdd0	mus musculu
14	37	84.1	112	2	Q8K1F2_MOUSE	Q8klf2	mus musculu
15	36	81.8	97	2	Q9JL76_MOUSE	Q9jl76	mus musculu
16	36	81.8	106	2	Q9U410_MOUSE	Q9u410	mus musculu
17	36	81.8	106	2	Q2VR04_MOUSE	Q2vr04	mus musculu
18	36	81.8	106	2	Q2VT25_MOUSE	Q2vt25	mus musculu
19	36	81.8	106	2	Q2VT27_MOUSE	Q2vt27	mus musculu
20	36	81.8	235	2	Q58EV6_MOUSE	Q58ev6	mus musculu
21	36	81.8	585	2	Q5CFX0_CRYHO	Q5cfx0	cryptospori
22	36	81.8	585	2	Q5CT89_CRYPV	Q5ct89	cryptospori
23	35	79.5	175	2	Q9YDM6_AERPE	Q9ydm6	aeropyrum p
24	35	79.5	351	2	Q4IPA6_GIBZE	Q4ipa6	gibberella
25	35	79.5	1055	2	Q5B7A9_EMENI	Q5b7a9	aspergillus
26	34	77.3	77	2	Q8VAH5_WSSV	Q8vah5	white spot
27	34	77.3	84	2	Q5CJT4_CRYHO	Q5cjt4	cryptospori
28	34	77.3	349	2	Q7Z4S8_HUMAN	Q7z4s8	homo sapien
29	34	77.3	377	1	Y835_METJA	Q58245	methanococc
30	34	77.3	409	2	Q3ATT0_CHLCH	Q3att0	chlorobium
31	34	77.3	420	2	Q8Z2N1_SALTI	Q8z2n1	salmonella
32	34	77.3	464	2	Q7XR50_ORYSA	Q7xr50	oryza sativ
33	34	77.3	543	2	Q4P336_USTMA	Q4p336	ustilago ma
34	34	77.3	568	2	Q2IRR9_RHOPA	Q2irr9	rhodopseudo
35	34	77.3	636	2	Q7YYR4_CRYPV	Q7yyr4	cryptospori
36	34	77.3	642	2	Q5CWU0_CRYPV	Q5cwu0	cryptospori
37	34	77.3	1788	2	Q9YGK0_OREAU	Q9ygm0	oreochromis
38	34	77.3	1800	2	Q8YYF0_ANASP	Q8yyf0	anabaena sp
39	33	75.0	106	2	Q2VT29_MOUSE	Q2vt29	mus musculu
40	33	75.0	184	2	Q8LF58_ARATH	Q8lf58	arabidopsis
41	33	75.0	209	2	Q470X4_RALEJ	Q470x4	ralstonia e
42	33	75.0	215	2	Q336X2_ORYSA	Q336x2	oryza sativ
43	33	75.0	219	2	Q8W2Y0_ORYSA	Q8w2y0	oryza sativ
44	33	75.0	235	2	Q5XFY8_MOUSE	Q5xfy8	mus musculu
45	33	75.0	261	2	Q50F30_9SALA	Q50f30	plethodon w
46	33	75.0	303	2	Q7YTL4_CAEEL	Q7ytl4	caenorhabdi
47	33	75.0	317	2	Q570M4_ARATH	Q570m4	arabidopsis
48	33	75.0	619	2	Q8YRD7_ANASP	Q8yrd7	anabaena sp
49	33	75.0	650	2	Q3M852_ANAVT	Q3m852	anabaena va
50	33	75.0	669	2	Q9SLC7_ARATH	Q9slc7	arabidopsis
51	33	75.0	716	2	Q5ATB3_EMENI	Q5atb3	aspergillus
52	33	75.0	837	2	Q2XY63_DROER	Q2xy63	drosophila
53	33	75.0	844	2	Q5B210_EMENI	Q5b210	aspergillus
54	33	75.0	1062	2	Q5ULI0_9CAUD	Q5uli0	lactobacill
55	33	75.0	1149	2	Q6C8L5_YARLI	Q6c8l5	yarrowia li
56	33	75.0	1284	2	Q4QIA3_LEIMA	Q4qia3	leishmania
57	32	72.7	42	2	Q8VVR9_STAAS	Q8vvr9	staphylococ
58	32	72.7	90	2	Q8H4N9_ORYSA	Q8h4n9	oryza sativ
59	32	72.7	126	2	Q7YBT5_9NEOP	Q7ybt5	lipeurus ca
60	32	72.7	144	2	Q2YW90_STAAB	Q2yw90	staphylococ
61	32	72.7	144	2	Q4L913_STAHL	Q4l913	staphylococ
62	32	72.7	144	2	Q5HD33_STAAC	Q5hd33	staphylococ
63	32	72.7	144	2	Q6G6F4_STAAS	Q6g6f4	staphylococ
64	32	72.7	144	2	Q6GDS5_STAAR	Q6gds5	staphylococ
65	32	72.7	144	2	Q79ZZ7_STAAS	Q79zz7	staphylococ

SCORE Search Results Details for Application 10661366 and Search Result us-10-661-366-4.closed.rag.

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OM protein - protein search, using sw model

Run on: August 9, 2006, 06:40:12 ; Search time 65.0656 Seconds
(without alignments)
49.189 Million cell updates/sec

Title: US-10-661-366-4
Perfect score: 32
Sequence: 1 TTSNLAS 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 837128

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Database : A_Geneseq_8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	32	100.0	7	9	ADY75169	Ady75169 Antibody
2	32	100.0	13	5	ADG67420	Adg67420 Mouse ant
3	32	100.0	13	5	ADG67422	Adg67422 Mouse ant
4	32	100.0	13	5	ADG67492	Adg67492 Humanised
5	32	100.0	13	5	ADG67421	Adg67421 Mouse ant
6	32	100.0	13	5	ADG67423	Adg67423 Mouse ant
7	32	100.0	13	5	ADG67491	Adg67491 Humanised
8	32	100.0	13	5	ADG67494	Adg67494 Humanised
9	32	100.0	13	5	ADG67424	Adg67424 Mouse ant
10	32	100.0	13	5	ADG67495	Adg67495 Humanised
11	32	100.0	13	5	ADG67493	Adg67493 Humanised
12	28	87.5	7	2	AAW41383	Aaw41383 CDR2 of 1
13	28	87.5	7	2	AAW73170	Aaw73170 CDR2 of 1
14	28	87.5	7	2	AAV28391	Aay28391 Peptide f
15	28	87.5	7	3	AAB10005	Aab10005 H. pylori
16	28	87.5	7	3	AAV97233	Aay97233 Complemen
17	28	87.5	7	4	AAB82707	Aab82707 VEGF anta
18	28	87.5	7	4	AAE13141	Aae13141 Humanised
19	28	87.5	7	4	AAB83164	Aab83164 Mouse gan
20	28	87.5	7	4	AAB81968	Aab81968 Gangliosi
21	28	87.5	7	4	AAG63992	Aag63992 Complemen
22	28	87.5	7	5	AAU81254	Aau81254 Murine tr
23	28	87.5	7	5	ABB98031	Abb98031 Zinc fing
24	28	87.5	7	5	ABB98067	Abb98067 Zinc fing
25	28	87.5	7	5	ABP49557	Abp49557 Zinc fing
26	28	87.5	7	5	ABP50607	Abp50607 Zinc fing
27	28	87.5	7	5	AAE25953	Aae25953 Mouse ant
28	28	87.5	7	5	AAU74410	Aau74410 Light cha
29	28	87.5	7	5	ABJ03804	Abj03804 Human VEG
30	28	87.5	7	6	ABJ26722	Abj26722 VEGF bind
31	28	87.5	7	6	ABO01100	Abo01100 Human VEG
32	28	87.5	7	6	ABO14464	Abol14464 Human VEG
33	28	87.5	7	7	ADA63790	Ada63790 Zinc fing
34	28	87.5	7	7	ADA64844	Ada64844 Zinc fing
35	28	87.5	7	7	ADM21745	Adm21745 Synthetic
36	28	87.5	7	7	ADM22281	Adm22281 Synthetic
37	28	87.5	7	8	ADE25807	Ade25807 Anti-alph
38	28	87.5	7	8	ADH59662	Adh59662 Light cha
39	28	87.5	7	8	ADH59683	Adh59683 Light cha
40	28	87.5	7	8	ADH77355	Adh77355 Yeast kil
41	28	87.5	7	8	ADK18199	Adk18199 Mouse VEG
42	28	87.5	7	8	ADS94371	Ads94371 Antibody
43	28	87.5	7	9	ADW14717	Adw14717 Monoclonal
44	28	87.5	7	9	ADZ52583	Adz52583 Mouse ant
45	28	87.5	7	9	AEA41149	Aea41149 Human leu
46	28	87.5	7	9	AEA44050	Aea44050 Anti-TPO
47	28	87.5	7	9	AEA99627	Aea99627 Human CAB
48	28	87.5	7	9	AED34770	Aed34770 Chimeric
49	28	87.5	7	9	AED65197	Aed65197 Light cha
50	28	87.5	7	9	AED55500	Aed55500 Human VEG
51	28	87.5	7	10	AEE10182	Aee10182 Human VEG
52	28	87.5	7	10	AEE98115	Aee98115 Murine PE
53	28	87.5	7	10	AEF24382	Aef24382 Mouse PAN
54	28	87.5	7	10	AEF45505	Aef45505 Zinc fing
55	28	87.5	7	10	AEF46059	Aef46059 Zinc fing
56	28	87.5	7	10	AEF48882	Aef48882 Zinc fing
57	28	87.5	7	10	AEF49436	Aef49436 Zinc fing

SCORE Search Results Details for Application 10661366 and Search Result us-10-661-366-4.closed.ra1.

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OM protein - protein search, using sw model

Run on: August 9, 2006, 07:02:53 ; Search time 17.2131 Seconds
(without alignments)
35.596 Million cell updates/sec

Title: US-10-661-366-4
Perfect score: 32
Sequence: 1 TTSNLAS 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 249102

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Database : Issued_Patents_AA:*
1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%	Query					
No.	Score	Match	Length	DB	ID	Description	

1	28	87.5	7	1	US-08-116-778E-10	Sequence 10, Appl
2	28	87.5	7	1	US-08-438-562-10	Sequence 10, Appl
3	28	87.5	7	1	US-08-483-528B-98	Sequence 98, Appl
4	28	87.5	7	2	US-09-171-945-27	Sequence 27, Appl
5	28	87.5	7	2	US-09-393-385B-109	Sequence 109, App
6	28	87.5	7	2	US-09-798-689-5	Sequence 5, Appli
7	28	87.5	7	2	US-10-195-752-109	Sequence 109, App
8	28	87.5	7	2	US-09-910-059-27	Sequence 27, Appl
9	28	87.5	7	3	US-10-006-069A-47	Sequence 47, Appl
10	28	87.5	7	3	US-09-990-186-1761	Sequence 1761, Ap
11	28	87.5	7	3	US-09-990-186-2815	Sequence 2815, Ap
12	27	84.4	7	1	US-07-946-421-2	Sequence 2, Appli
13	27	84.4	7	2	US-08-783-853A-13	Sequence 13, Appl
14	27	84.4	7	2	US-09-280-028-14	Sequence 14, Appl
15	27	84.4	7	2	US-09-344-050-13	Sequence 13, Appl
16	27	84.4	7	2	US-09-091-071-4	Sequence 4, Appli
17	27	84.4	7	2	US-09-563-222C-36	Sequence 36, Appl
18	27	84.4	7	2	US-09-339-596A-38	Sequence 38, Appl
19	27	84.4	7	2	US-09-453-718B-19	Sequence 19, Appl
20	25	78.1	10	3	US-09-641-528B-243	Sequence 243, App
21	25	78.1	10	3	US-09-641-528B-12286	Sequence 12286, A
22	25	78.1	10	3	US-09-641-528B-20707	Sequence 20707, A
23	25	78.1	10	3	US-09-641-528B-30505	Sequence 30505, A
24	25	78.1	10	3	US-09-641-528B-32367	Sequence 32367, A
25	25	78.1	10	3	US-09-641-528B-40394	Sequence 40394, A
26	25	78.1	11	3	US-09-641-528B-207	Sequence 207, App
27	25	78.1	11	3	US-09-641-528B-244	Sequence 244, App
28	25	78.1	11	3	US-09-641-528B-12287	Sequence 12287, A
29	25	78.1	11	3	US-09-641-528B-20651	Sequence 20651, A
30	25	78.1	11	3	US-09-641-528B-20708	Sequence 20708, A
31	25	78.1	11	3	US-09-641-528B-30490	Sequence 30490, A
32	25	78.1	11	3	US-09-641-528B-32210	Sequence 32210, A
33	25	78.1	11	3	US-09-641-528B-32368	Sequence 32368, A
34	25	78.1	11	3	US-09-641-528B-40300	Sequence 40300, A
35	25	78.1	15	2	US-09-947-372A-31	Sequence 31, Appl
36	25	78.1	15	3	US-09-641-528B-46563	Sequence 46563, A
37	24	75.0	7	2	US-09-716-637-27	Sequence 27, Appl
38	24	75.0	7	3	US-09-844-508-3	Sequence 3, Appli
39	24	75.0	7	3	US-10-006-069A-43	Sequence 43, Appl
40	24	75.0	7	3	US-10-006-069A-44	Sequence 44, Appl
41	24	75.0	7	3	US-10-006-069A-45	Sequence 45, Appl
42	24	75.0	7	3	US-10-006-069A-161	Sequence 161, App
43	24	75.0	7	3	US-09-990-186-193	Sequence 193, App
44	24	75.0	7	3	US-09-990-186-194	Sequence 194, App
45	24	75.0	7	3	US-09-990-186-195	Sequence 195, App
46	24	75.0	7	3	US-09-990-186-730	Sequence 730, App
47	24	75.0	7	3	US-09-990-186-731	Sequence 731, App
48	24	75.0	7	3	US-09-990-186-732	Sequence 732, App
49	24	75.0	7	3	US-09-990-186-814	Sequence 814, App
50	24	75.0	7	3	US-09-990-186-815	Sequence 815, App
51	24	75.0	7	3	US-09-990-186-824	Sequence 824, App
52	24	75.0	7	3	US-09-990-186-850	Sequence 850, App
53	24	75.0	7	3	US-09-990-186-2857	Sequence 2857, Ap
54	24	75.0	7	3	US-09-990-186-3499	Sequence 3499, Ap
55	24	75.0	9	3	US-09-641-528B-20719	Sequence 20719, A
56	24	75.0	9	3	US-09-641-528B-32383	Sequence 32383, A
57	24	75.0	9	3	US-09-641-528B-40406	Sequence 40406, A
58	24	75.0	10	3	US-09-641-528B-20720	Sequence 20720, A
59	24	75.0	10	3	US-09-641-528B-32384	Sequence 32384, A
60	24	75.0	14	1	US-08-672-345C-31	Sequence 31, Appl
61	24	75.0	14	1	US-08-672-345C-34	Sequence 34, Appl

SCORE Search Results Details for Application 10661366 and Search Result us-10-661-366-4.closed.rapbm.

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OM protein - protein search, using sw model

Run on: August 9, 2006, 07:35:38 ; Search time 55.6557 Seconds
(without alignments)
58.260 Million cell updates/sec

Title: US-10-661-366-4
Perfect score: 32
Sequence: 1 TTSNLAS 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 395127

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Database : Published_Applications_AA_Main:*
1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	32	100.0	7	5 US-10-661-366-4	Sequence 4, Appli

2	32	100.0	13	4	US-10-468-496-1912	Sequence 1912, Ap
3	32	100.0	13	4	US-10-468-496-1913	Sequence 1913, Ap
4	32	100.0	13	4	US-10-468-496-1914	Sequence 1914, Ap
5	32	100.0	13	4	US-10-468-496-1915	Sequence 1915, Ap
6	32	100.0	13	4	US-10-468-496-1916	Sequence 1916, Ap
7	32	100.0	13	4	US-10-468-496-1983	Sequence 1983, Ap
8	32	100.0	13	4	US-10-468-496-1984	Sequence 1984, Ap
9	32	100.0	13	4	US-10-468-496-1985	Sequence 1985, Ap
10	32	100.0	13	4	US-10-468-496-1986	Sequence 1986, Ap
11	32	100.0	13	4	US-10-468-496-1987	Sequence 1987, Ap
12	28	87.5	7	3	US-09-976-787-5	Sequence 5, Appli
13	28	87.5	7	3	US-09-865-198-5	Sequence 5, Appli
14	28	87.5	7	3	US-09-910-059-27	Sequence 27, Appl
15	28	87.5	7	3	US-09-846-033B-47	Sequence 47, Appl
16	28	87.5	7	3	US-09-990-186-1761	Sequence 1761, Ap
17	28	87.5	7	3	US-09-990-186-2815	Sequence 2815, Ap
18	28	87.5	7	3	US-09-798-689-5	Sequence 5, Appli
19	28	87.5	7	3	US-09-989-994-1761	Sequence 1761, Ap
20	28	87.5	7	3	US-09-989-994-2815	Sequence 2815, Ap
21	28	87.5	7	3	US-09-842-776A-20	Sequence 20, Appl
22	28	87.5	7	4	US-10-006-069A-47	Sequence 47, Appl
23	28	87.5	7	4	US-10-195-752-109	Sequence 109, App
24	28	87.5	7	4	US-10-232-187-9	Sequence 9, Appli
25	28	87.5	7	4	US-10-461-878-2	Sequence 2, Appli
26	28	87.5	7	4	US-10-433-258-65	Sequence 65, Appl
27	28	87.5	7	4	US-10-433-258-104	Sequence 104, App
28	28	87.5	7	4	US-10-312-316-26	Sequence 26, Appl
29	28	87.5	7	5	US-10-482-630-5	Sequence 5, Appli
30	28	87.5	7	5	US-10-203-399B-5	Sequence 5, Appli
31	28	87.5	7	5	US-10-778-910-5	Sequence 5, Appli
32	28	87.5	7	5	US-10-461-885-2	Sequence 2, Appli
33	28	87.5	7	5	US-10-687-035-70	Sequence 70, Appl
34	28	87.5	7	5	US-10-809-387-5	Sequence 5, Appli
35	28	87.5	7	5	US-10-507-662-14	Sequence 14, Appl
36	28	87.5	7	6	US-11-101-287-47	Sequence 47, Appl
37	28	87.5	7	6	US-11-115-922-47	Sequence 47, Appl
38	28	87.5	7	6	US-11-225-686-1761	Sequence 1761, Ap
39	28	87.5	7	6	US-11-225-686-2815	Sequence 2815, Ap
40	28	87.5	7	6	US-11-202-009-1761	Sequence 1761, Ap
41	28	87.5	7	6	US-11-202-009-2815	Sequence 2815, Ap
42	28	87.5	8	4	US-10-018-245A-5	Sequence 5, Appli
43	28	87.5	8	6	US-11-097-812-129	Sequence 129, App
44	28	87.5	13	4	US-10-468-496-1911	Sequence 1911, Ap
45	27	84.4	7	3	US-09-965-099-13	Sequence 13, Appl
46	27	84.4	7	3	US-09-563-222-36	Sequence 36, Appl
47	27	84.4	7	3	US-09-791-551-25	Sequence 25, Appl
48	27	84.4	7	4	US-10-051-852-13	Sequence 13, Appl
49	27	84.4	7	4	US-10-160-232-19	Sequence 19, Appl
50	27	84.4	7	4	US-10-071-962-25	Sequence 25, Appl
51	27	84.4	7	4	US-10-230-880-116	Sequence 116, App
52	27	84.4	7	4	US-10-344-779-6	Sequence 6, Appli
53	27	84.4	7	4	US-10-366-709-4	Sequence 4, Appli
54	27	84.4	7	4	US-10-430-176-13	Sequence 13, Appl
55	27	84.4	7	4	US-10-449-566-75	Sequence 75, Appl
56	27	84.4	7	4	US-10-449-566-84	Sequence 84, Appl
57	27	84.4	7	4	US-10-239-656-20	Sequence 20, Appl
58	27	84.4	7	4	US-10-327-663-6	Sequence 6, Appli
59	27	84.4	7	4	US-10-681-421-13	Sequence 13, Appl
60	27	84.4	7	4	US-10-738-809-6	Sequence 6, Appli
61	27	84.4	7	4	US-10-783-950-36	Sequence 36, Appl
62	27	84.4	7	5	US-10-849-615-7	Sequence 7, Appli

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Page	List	Overview	FAQ	Suggestions

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OM protein - protein search, using sw model

Run on: August 9, 2006, 07:36:48 ; Search time 8.83607 Seconds
(without alignments)
53.325 Million cell updates/sec

Title: US-10-661-366-4
Perfect score: 32
Sequence: 1 TTSNLAS 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 239914 seqs, 67312017 residues

Total number of hits satisfying chosen parameters: 27373

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Database : Published_Applications_AA_New:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	% Query
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No.	Score	Match	Length	DB	ID	Description
1	28	87.5	11	6	US-10-522-086-22	Sequence 22, Appl
2	28	87.5	11	6	US-10-542-682-42	Sequence 42, Appl
3	28	87.5	11	6	US-10-542-682-56	Sequence 56, Appl
4	24	75.0	7	7	US-11-376-338-13	Sequence 13, Appl
5	22	68.8	7	7	US-11-254-182-58	Sequence 58, Appl
6	22	68.8	7	7	US-11-106-762-21	Sequence 21, Appl
7	22	68.8	7	7	US-11-291-698A-45	Sequence 45, Appl
8	22	68.8	9	7	US-11-099-283B-45	Sequence 45, Appl
9	22	68.8	9	7	US-11-099-283B-608	Sequence 608, App
10	22	68.8	13	7	US-11-134-871-133	Sequence 133, App
11	21	65.6	7	6	US-10-513-148A-9	Sequence 9, Appli
12	21	65.6	7	7	US-11-263-230-5	Sequence 5, Appli
13	21	65.6	7	7	US-11-263-230-105	Sequence 105, App
14	21	65.6	7	7	US-11-263-230-123	Sequence 123, App
15	21	65.6	7	7	US-11-301-373-9	Sequence 9, Appli
16	21	65.6	12	7	US-11-375-551-37	Sequence 37, Appl
17	20	62.5	9	7	US-11-140-487A-879	Sequence 879, App
18	20	62.5	9	7	US-11-140-487A-1878	Sequence 1878, Ap
19	20	62.5	9	7	US-11-140-487A-1879	Sequence 1879, Ap
20	20	62.5	10	7	US-11-140-487A-2029	Sequence 2029, Ap
21	20	62.5	11	7	US-11-045-488-20	Sequence 20, Appl
22	20	62.5	13	7	US-11-134-871-1998	Sequence 1998, Ap
23	19	59.4	7	7	US-11-263-230-81	Sequence 81, Appl
24	19	59.4	7	7	US-11-263-230-143	Sequence 143, App
25	19	59.4	9	6	US-10-538-066-55	Sequence 55, Appl
26	19	59.4	11	7	US-11-259-133-139	Sequence 139, App
27	19	59.4	11	7	US-11-259-133-169	Sequence 169, App
28	19	59.4	11	7	US-11-259-133-175	Sequence 175, App
29	19	59.4	11	7	US-11-259-133-199	Sequence 199, App
30	19	59.4	12	6	US-10-967-088-58	Sequence 58, Appl
31	19	59.4	13	6	US-10-614-959-13	Sequence 13, Appl
32	19	59.4	15	6	US-10-537-642-1085	Sequence 1085, Ap
33	18	56.2	7	7	US-11-263-230-124	Sequence 124, App
34	18	56.2	7	7	US-11-263-230-137	Sequence 137, App
35	18	56.2	7	7	US-11-263-230-165	Sequence 165, App
36	18	56.2	7	7	US-11-263-230-550	Sequence 550, App
37	18	56.2	7	7	US-11-263-230-572	Sequence 572, App
38	18	56.2	7	7	US-11-263-230-615	Sequence 615, App
39	18	56.2	7	7	US-11-061-841-76	Sequence 76, Appl
40	18	56.2	9	7	US-11-140-487A-1706	Sequence 1706, Ap
41	18	56.2	12	6	US-10-520-470-58	Sequence 58, Appl
42	18	56.2	12	7	US-11-134-871-1125	Sequence 1125, Ap
43	18	56.2	13	6	US-10-991-309B-97	Sequence 97, Appl
44	18	56.2	14	7	US-11-134-871-1863	Sequence 1863, Ap
45	17	53.1	6	7	US-11-054-072-8622	Sequence 8622, Ap
46	17	53.1	7	6	US-10-499-266-9	Sequence 9, Appli
47	17	53.1	7	7	US-11-023-959A-56	Sequence 56, Appl
48	17	53.1	7	7	US-11-263-230-535	Sequence 535, App
49	17	53.1	7	7	US-11-263-230-554	Sequence 554, App
50	17	53.1	7	7	US-11-263-230-577	Sequence 577, App
51	17	53.1	7	7	US-11-263-230-1211	Sequence 1211, Ap
52	17	53.1	7	7	US-11-263-230-1235	Sequence 1235, Ap
53	17	53.1	7	7	US-11-263-230-1259	Sequence 1259, Ap
54	17	53.1	7	7	US-11-196-917A-69	Sequence 69, Appl
55	17	53.1	10	6	US-10-516-079-66	Sequence 66, Appl
56	17	53.1	10	6	US-10-526-062-24	Sequence 24, Appl
57	17	53.1	10	6	US-10-522-810-66	Sequence 66, Appl
58	17	53.1	11	6	US-10-542-682-45	Sequence 45, Appl
59	17	53.1	11	7	US-11-194-051-4	Sequence 4, Appli

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OM protein - protein search, using sw model

Run on: August 9, 2006, 06:51:47 ; Search time 9.63934 Seconds
(without alignments)
69.872 Million cell updates/sec

Title: US-10-661-366-4
Perfect score: 32
Sequence: 1 TTSNLAS 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 2523

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	19	59.4	15	2 A56970	GLYMA1 - soybean (
2	18	56.2	15	2 I50503	agrin - electric r
3	16	50.0	10	2 PH0894	T-cell receptor be
4	16	50.0	10	2 S27873	hypothetical prote
5	16	50.0	13	2 PC2369	unidentified 85K p
6	16	50.0	14	2 A61306	ribonuclease M (EC
7	16	50.0	15	2 B61243	dimethylaniline mo
8	15	46.9	9	2 A28924	fructose-bisphosph

9	15	46.9	10	2	PA0050	protein QA100052 -
10	15	46.9	14	2	B39111	Ig heavy chain V r
11	15	46.9	15	2	PH1616	Ig H chain V-D-J r
12	15	46.9	15	2	A08416	lombicine kinase
13	14	43.8	9	2	JP0073	ribosomal protein
14	14	43.8	10	2	A47364	placental lactogen
15	14	43.8	10	2	S30348	clotting protein -
16	14	43.8	11	2	S69349	neuropeptide FFami
17	14	43.8	12	2	S36902	Em protein - wheat
18	14	43.8	13	2	S47381	T-cell antigen rec
19	14	43.8	13	2	S13273	polysialoglycoprot
20	14	43.8	14	2	A35377	GTP-binding protei
21	14	43.8	14	2	I64815	carbonic anhydrase
22	14	43.8	14	2	PH1768	T cell receptor al
23	14	43.8	14	2	PH1628	Ig H chain V-D-J r
24	14	43.8	14	2	A44515	Trp EG leader pept
25	14	43.8	15	2	E49037	TcR delta chain V-
26	14	43.8	15	2	PL0154	glycoprotein - log
27	13	40.6	5	2	A37114	hypoxanthine phosph
28	13	40.6	8	2	S68802	nitrate reductase
29	13	40.6	9	2	PH0902	T-cell receptor be
30	13	40.6	9	2	JQ0914	MHC class I histoc
31	13	40.6	10	2	S74176	gluconokinase (EC
32	13	40.6	12	2	S17540	agglutinin-III lec
33	13	40.6	12	2	A28955	polysialoglycoprot
34	13	40.6	12	4	PC2123	aminotransferase c
35	13	40.6	12	4	S49073	frame shifted cyta
36	13	40.6	13	2	B28955	polysialoglycoprot
37	13	40.6	14	2	S36678	dodecenoyl-CoA Del
38	13	40.6	15	2	B26997	unspecific monooxy
39	13	40.6	15	2	S26531	T-cell receptor al
40	13	40.6	15	2	PA0029	protein QA100012 -
41	13	40.6	15	2	D38925	seed storage prote
42	13	40.6	15	2	PH1631	Ig H chain V-D-J r
43	13	40.6	15	2	PH0752	T-cell receptor be
44	13	40.6	15	2	D54226	light-harvesting p
45	12	37.5	6	2	S14159	parasporal crystal
46	12	37.5	7	2	A25269	sex pheromone cAM3
47	12	37.5	9	2	C41170	photosystem II pro
48	12	37.5	9	2	S65865	collagen alpha 2(V
49	12	37.5	9	2	JQ1202	leader peptide - P
50	12	37.5	10	2	C61440	polygalacturonase
51	12	37.5	10	2	S70722	65.4K GTP-binding
52	12	37.5	10	2	A59272	peptide-N4-(N-acet
53	12	37.5	11	2	B41835	translation elonga
54	12	37.5	11	2	S45386	low density lipopr
55	12	37.5	12	2	A55837	5-aminoimidazole r
56	12	37.5	12	2	PT0216	T-cell receptor be
57	12	37.5	12	2	PH1464	T-cell receptor be
58	12	37.5	12	2	A44874	proboscipedia - fr
59	12	37.5	13	2	S36874	cytochrome P450 CM
60	12	37.5	13	2	PU0038	alpha-peptide/alg
61	12	37.5	13	2	PC1149	equinatoxin 1A - s
62	12	37.5	13	2	PH0138	T-cell receptor be
63	12	37.5	13	2	A40207	cell surface glyco
64	12	37.5	13	2	S04013	lignin peroxidase
65	12	37.5	13	2	S04014	lignin peroxidase
66	12	37.5	13	2	S32471	lymnaDFamide 1 - g
67	12	37.5	13	2	S32474	lymnaDFamide 4 - g
68	12	37.5	14	2	PL0152	metal-binding prot
69	12	37.5	14	2	PT0259	Ig heavy chain CRD

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OM protein - protein search, using sw model

Run on: August 9, 2006, 06:40:52 ; Search time 78.0328 Seconds
(without alignments)
82.979 Million cell updates/sec

Title: US-10-661-366-4
Perfect score: 32
Sequence: 1 TTSNLAS 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 8966

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Database : UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	23	71.9	13	2	Q9SB03_ORYSA	Q9sb03 oryza sativ
2	19	59.4	10	1	COCIN_PHACN	P84785 phaseolus c
3	19	59.4	10	2	Q4X3I4_PLACH	Q4x3i4 plasmodium
4	19	59.4	12	2	Q9TTE3_PIG	Q9tte3 sus scrofa

5	19	59.4	15	2	Q9UEM3_HUMAN	Q9uem3	homo sapien
6	19	59.4	15	2	Q7M285_SOYBN	Q7m285	glycine max
7	18	56.2	8	2	Q7Z7I9_HUMAN	Q7z7i9	homo sapien
8	18	56.2	9	2	Q8W7U0_BOSCA	Q8w7u0	bostrychia
9	18	56.2	10	1	GYMN_GYMCH	P84200	gymnocladus
10	18	56.2	11	2	O68237_BORBU	O68237	borrelia bu
11	18	56.2	12	2	Q9SPT5_PEA	Q9spt5	pisum sativ
12	18	56.2	15	2	Q9WTA3_9ARAE	Q9wta3	amorphophal
13	18	56.2	15	2	Q90403_DISOM	Q90403	discopyge o
14	17	53.1	8	2	P77556_ECOLI	P77556	escherichia
15	17	53.1	10	2	Q8GUV6_9BRAS	Q8guv6	capsella ru
16	17	53.1	14	2	Q6GWV6_SHEEP	Q6gww6	ovis aries
17	17	53.1	15	1	CWP03_DAUCA	P80753	daucus caro
18	17	53.1	15	2	Q6GWV7_BOVIN	Q6gww7	bos taurus
19	16	50.0	9	2	Q76FU1_9FLOR	Q76ful	plocamium t
20	16	50.0	9	2	Q76FU5_9FLOR	Q76fu5	plocamium s
21	16	50.0	9	2	Q76FU7_9FLOR	Q76fu7	plocamium r
22	16	50.0	9	2	Q76FV1_9FLOR	Q76fv1	plocamium o
23	16	50.0	9	2	Q76FV7_PLOCA	Q76fv7	plocamium c
24	16	50.0	10	2	Q61807_MOUSE	Q61807	mus musculus
25	16	50.0	11	2	Q80B26_HBV	Q80b26	hepatitis b
26	16	50.0	13	1	UN41_CLOPA	P81360	clostridium
27	16	50.0	13	2	Q7M0L4_BACCE	Q7m0l4	bacillus ce
28	16	50.0	14	1	TE1LB_RANLU	P82831	rana luteiv
29	16	50.0	14	2	Q7M4U3_9EURO	Q7m4u3	aspergillus
30	16	50.0	14	2	Q9MRF6_9POAL	Q9mrf6	hordeum mur
31	16	50.0	14	2	Q44787_BORBU	Q44787	borrelia bu
32	16	50.0	14	2	Q8V1H7_HBV	Q8vlh7	hepatitis b
33	16	50.0	15	1	GSTE2_PSEUO	P83000	pseudomonas
34	16	50.0	15	2	Q9QVJ2_9MURI	Q9qvj2	rattus sp.
35	15	46.9	7	2	Q65578_9ALPH	Q65578	bovine herp
36	15	46.9	8	2	Q3BDS9_HORSE	Q3bds9	equus cabal
37	15	46.9	8	2	Q58U13_SECST	Q58ul3	secale stri
38	15	46.9	8	2	Q58U18_PSAFR	Q58ul8	psathyrosta
39	15	46.9	8	2	Q58U49_9POAL	Q58u49	australopyr
40	15	46.9	9	2	Q7M2K6_RABIT	Q7m2k6	oryctolagus
41	15	46.9	9	2	Q58U35_FESSE	Q58u35	festucopsis
42	15	46.9	9	2	Q58U41_9POAL	Q58u41	haynaldia v
43	15	46.9	9	2	Q5SBX0_9POAL	Q5sbx0	restio insi
44	15	46.9	9	2	Q8RKU3_BORBU	Q8rku3	borrelia bu
45	15	46.9	10	2	Q58U15_PSAST	Q58ul5	psathyrosta
46	15	46.9	10	2	Q58U20_CRIDE	Q58u20	crithopsis
47	15	46.9	10	2	Q58U37_9POAL	Q58u37	eremopyrum
48	15	46.9	10	2	Q58U47_9POAL	Q58u47	australopyr
49	15	46.9	10	2	Q58U54_BROST	Q58u54	bromus ster
50	15	46.9	10	2	Q5SBS2_9POAL	Q5sbs2	thamnochort
51	15	46.9	11	1	ATPE_POPEU	P84559	populus eup
52	15	46.9	11	2	Q58U09_TAECM	Q58u09	taeniatheru
53	15	46.9	11	2	Q58U22_9POAL	Q58u22	peridictyon
54	15	46.9	11	2	Q58U24_AEGTA	Q58u24	aegilops ta
55	15	46.9	11	2	Q58U26_LOPEL	Q58u26	lophopyrum
56	15	46.9	11	2	Q58U43_TRIMO	Q58u43	triticum mo
57	15	46.9	11	2	Q58U51_9POAL	Q58u51	amblyopyrum
58	15	46.9	11	2	Q5SBQ8_9POAL	Q5sbq8	thamnochort
59	15	46.9	11	2	Q5SBW8_9POAL	Q5sbw8	restio simi
60	15	46.9	12	2	Q58U39_EREDI	Q58u39	eremopyrum
61	15	46.9	12	2	Q58U56_BROAV	Q58u56	bromus arve
62	15	46.9	12	2	Q9QVF2_9MURI	Q9qv2	rattus sp.
63	15	46.9	12	2	Q9WUX1_RAT	Q9wux1	rattus norv
64	15	46.9	13	2	Q7RDQ1_PLAYO	Q7rdq1	plasmodium
65	15	46.9	13	2	Q94IJ0_MAIZE	Q94ij0	zea mays (m

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OM protein - protein search, using sw model

Run on: August 9, 2006, 07:45:18 ; Search time 17.6792 Seconds
(without alignments)
181.033 Million cell updates/sec

Title: US-10-661-366-4
Perfect score: 32
Sequence: 1 TTSNLAS 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : A_Geneseq_8:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*
- 9: geneseqp2005s:*
- 10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	32	100.0	7	9	ADY75169	Ady75169 Antibody
2	32	100.0	13	5	ADG67420	Adg67420 Mouse ant
3	32	100.0	13	5	ADG67422	Adg67422 Mouse ant
4	32	100.0	13	5	ADG67492	Adg67492 Humanised
5	32	100.0	13	5	ADG67421	Adg67421 Mouse ant
6	32	100.0	13	5	ADG67423	Adg67423 Mouse ant
7	32	100.0	13	5	ADG67491	Adg67491 Humanised
8	32	100.0	13	5	ADG67494	Adg67494 Humanised
9	32	100.0	13	5	ADG67424	Adg67424 Mouse ant
10	32	100.0	13	5	ADG67495	Adg67495 Humanised
11	32	100.0	13	5	ADG67493	Adg67493 Humanised
12	32	100.0	106	2	AAR24105	Aar24105 Anti-Tac
13	32	100.0	106	2	AAR38616	Aar38616 Modified
14	32	100.0	106	2	AAW58508	Aaw58508 Protein S
15	32	100.0	106	2	AAW58511	Aaw58511 Protein S
16	32	100.0	106	2	AAW58512	Aaw58512 Protein S
17	32	100.0	106	2	AAW37813	Aaw37813 Humanized
18	32	100.0	106	4	AAB69651	Aab69651 Murine an
19	32	100.0	106	4	AAB69648	Aab69648 Humanised
20	32	100.0	106	4	AAB69647	Aab69647 Humanised
21	32	100.0	106	4	AAB69641	Aab69641 Murine an
22	32	100.0	106	5	ABJ10393	Abj10393 Disulphid
23	32	100.0	106	5	ABJ10395	Abj10395 Mutant an
24	32	100.0	106	5	ABJ10394	Abj10394 Mutant an
25	32	100.0	106	8	ADI01225	Adi01225 Murine an
26	32	100.0	106	8	ADI01224	Adi01224 Protein s
27	32	100.0	106	8	ADI01191	Adi01191 Murine an
28	32	100.0	106	8	ADO47704	Ado47704 Mouse ant
29	32	100.0	106	8	ADO47730	Ado47730 PDL-only
30	32	100.0	106	8	ADO47731	Ado47731 CDR-only
31	32	100.0	106	9	AEB12544	Aeb12544 Antibody
32	32	100.0	106	9	AEB12558	Aeb12558 Humanized
33	32	100.0	107	9	ADY75167	Ady75167 Antibody
34	32	100.0	110	2	AAW46482	Aaw46482 SIC5 VK a
35	32	100.0	113	4	AAB48936	Aab48936 Anti-TrkA
36	32	100.0	126	2	AAR24108	Aar24108 Humanised
37	32	100.0	126	2	AAR06375	Aar06375 Anti-Tac
38	32	100.0	126	4	AAB69654	Aab69654 Humanised
39	32	100.0	126	8	ADO47737	Ado47737 Humanisd
40	32	100.0	128	1	AAP93150	Aap93150 Protein e
41	32	100.0	128	6	ABJ39021	Abj39021 Murine an
42	32	100.0	213	8	ADT51685	Adt51685 Daclizuma
43	32	100.0	213	10	AEF16400	Aef16400 Humanized
44	32	100.0	215	8	ADN97547	Adn97547 Artificia
45	32	100.0	236	2	AAR45442	Aar45442 Sequence
46	32	100.0	237	2	AAR94020	Aar94020 Anti-erbB
47	32	100.0	237	2	AAW15185	Aaw15185 Single-ch
48	32	100.0	237	3	AAW79059	Aay79059 Amino aci
49	32	100.0	239	3	AAB12563	Aab12563 Anti-TAC
50	32	100.0	239	4	AAB36826	Aab36826 Anti-TAC
51	32	100.0	239	7	ADC79231	Adc79231 Anti-CA12
52	32	100.0	239	7	ADC79232	Adc79232 Control s
53	32	100.0	290	9	AEB30749	Aeb30749 CD20 EC d
54	32	100.0	295	4	AAB48934	Aab48934 Anti-TrkA
55	32	100.0	319	9	AEB30747	Aeb30747 CD20 EC d
56	32	100.0	438	6	ABJ39019	Abj39019 Anti-TAC
57	32	100.0	483	8	ADN97549	Adn97549 Artificia

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OM protein - protein search, using sw model

Run on: August 9, 2006, 08:17:00 ; Search time 4.61092 Seconds
(without alignments)
132.883 Million cell updates/sec

Title: US-10-661-366-4
Perfect score: 32
Sequence: 1 TTSNLAS 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Issued_Patents_AA:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
------------	-------	--------------------	----	-------------

1	32	100.0	106	1	US-07-634-278-1	Sequence 1, Appli
2	32	100.0	106	1	US-07-634-278-7	Sequence 7, Appli
3	32	100.0	106	1	US-07-634-278-8	Sequence 8, Appli
4	32	100.0	106	1	US-07-634-278-16	Sequence 16, Appl
5	32	100.0	106	1	US-08-477-728-1	Sequence 1, Appli
6	32	100.0	106	1	US-08-477-728-7	Sequence 7, Appli
7	32	100.0	106	1	US-08-477-728-8	Sequence 8, Appli
8	32	100.0	106	1	US-08-477-728-16	Sequence 16, Appl
9	32	100.0	106	1	US-08-474-040-1	Sequence 1, Appli
10	32	100.0	106	1	US-08-474-040-7	Sequence 7, Appli
11	32	100.0	106	1	US-08-474-040-8	Sequence 8, Appli
12	32	100.0	106	1	US-08-474-040-16	Sequence 16, Appl
13	32	100.0	106	1	US-08-487-200-1	Sequence 1, Appli
14	32	100.0	106	1	US-08-487-200-7	Sequence 7, Appli
15	32	100.0	106	1	US-08-487-200-8	Sequence 8, Appli
16	32	100.0	106	1	US-08-487-200-16	Sequence 16, Appl
17	32	100.0	106	1	US-08-488-113B-163	Sequence 163, App
18	32	100.0	106	1	US-08-488-113B-164	Sequence 164, App
19	32	100.0	106	1	US-08-488-113B-165	Sequence 165, App
20	32	100.0	106	1	US-08-477-484B-163	Sequence 163, App
21	32	100.0	106	1	US-08-477-484B-164	Sequence 164, App
22	32	100.0	106	1	US-08-477-484B-165	Sequence 165, App
23	32	100.0	106	1	US-08-107-669D-49	Sequence 49, Appl
24	32	100.0	106	1	US-08-107-669D-50	Sequence 50, Appl
25	32	100.0	106	1	US-08-107-669D-51	Sequence 51, Appl
26	32	100.0	106	1	US-08-472-788A-50	Sequence 50, Appl
27	32	100.0	106	1	US-08-472-788A-83	Sequence 83, Appl
28	32	100.0	106	1	US-08-472-788A-84	Sequence 84, Appl
29	32	100.0	106	1	US-08-477-531B-49	Sequence 49, Appl
30	32	100.0	106	1	US-08-477-531B-50	Sequence 50, Appl
31	32	100.0	106	1	US-08-477-531B-51	Sequence 51, Appl
32	32	100.0	106	1	US-08-646-360-163	Sequence 163, App
33	32	100.0	106	1	US-08-646-360-164	Sequence 164, App
34	32	100.0	106	1	US-08-646-360-165	Sequence 165, App
35	32	100.0	106	1	US-08-082-842A-50	Sequence 50, Appl
36	32	100.0	106	1	US-08-082-842A-83	Sequence 83, Appl
37	32	100.0	106	1	US-08-082-842A-84	Sequence 84, Appl
38	32	100.0	106	2	US-08-934-841-2	Sequence 2, Appli
39	32	100.0	106	2	US-09-393-409-2	Sequence 2, Appli
40	32	100.0	106	2	US-08-839-765-163	Sequence 163, App
41	32	100.0	106	2	US-08-839-765-164	Sequence 164, App
42	32	100.0	106	2	US-08-839-765-165	Sequence 165, App
43	32	100.0	106	2	US-09-136-389-163	Sequence 163, App
44	32	100.0	106	2	US-09-136-389-164	Sequence 164, App
45	32	100.0	106	2	US-09-136-389-165	Sequence 165, App
46	32	100.0	106	2	US-08-484-537-1	Sequence 1, Appli
47	32	100.0	106	2	US-08-484-537-7	Sequence 7, Appli
48	32	100.0	106	2	US-08-484-537-8	Sequence 8, Appli
49	32	100.0	106	2	US-08-484-537-16	Sequence 16, Appl
50	32	100.0	106	2	US-09-610-838-163	Sequence 163, App
51	32	100.0	106	2	US-09-610-838-164	Sequence 164, App
52	32	100.0	106	2	US-09-610-838-165	Sequence 165, App
53	32	100.0	106	2	US-09-711-485-163	Sequence 163, App
54	32	100.0	106	2	US-09-711-485-164	Sequence 164, App
55	32	100.0	106	2	US-09-711-485-165	Sequence 165, App
56	32	100.0	106	3	US-09-718-998-1	Sequence 1, Appli
57	32	100.0	106	3	US-09-718-998-7	Sequence 7, Appli
58	32	100.0	106	3	US-09-718-998-8	Sequence 8, Appli
59	32	100.0	106	3	US-09-718-998-16	Sequence 16, Appl
60	32	100.0	126	1	US-07-634-278-21	Sequence 21, Appl

SCORE Search Results Details for Application 10661366 and Search Result us-10-661-366-4.ra

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This page gives you Search Results detail for the Application 10661366 and Search Result us-10-661-366-4.ra.pbm.

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OM protein - protein search, using sw model

Run on: August 9, 2006, 09:01:05 ; Search time 14.9795 Seconds
(without alignments)
216.462 Million cell updates/sec

Title: US-10-661-366-4
Perfect score: 32
Sequence: 1 TTSNLAS 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Published_Applications_AA_Main:*
1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	32	100.0	7	5	US-10-661-366-4	Sequence 4, Appli
2	32	100.0	13	4	US-10-468-496-1912	Sequence 1912, Ap
3	32	100.0	13	4	US-10-468-496-1913	Sequence 1913, Ap

4	32	100.0	13	4	US-10-468-496-1914	Sequence 1914, Ap
5	32	100.0	13	4	US-10-468-496-1915	Sequence 1915, Ap
6	32	100.0	13	4	US-10-468-496-1916	Sequence 1916, Ap
7	32	100.0	13	4	US-10-468-496-1983	Sequence 1983, Ap
8	32	100.0	13	4	US-10-468-496-1984	Sequence 1984, Ap
9	32	100.0	13	4	US-10-468-496-1985	Sequence 1985, Ap
10	32	100.0	13	4	US-10-468-496-1986	Sequence 1986, Ap
11	32	100.0	13	4	US-10-468-496-1987	Sequence 1987, Ap
12	32	100.0	106	4	US-10-127-890-163	Sequence 163, App
13	32	100.0	106	4	US-10-127-890-164	Sequence 164, App
14	32	100.0	106	4	US-10-127-890-165	Sequence 165, App
15	32	100.0	106	4	US-10-340-189-50	Sequence 50, Appl
16	32	100.0	106	4	US-10-340-189-83	Sequence 83, Appl
17	32	100.0	106	4	US-10-340-189-84	Sequence 84, Appl
18	32	100.0	106	4	US-10-389-155-1	Sequence 1, Appli
19	32	100.0	106	4	US-10-389-155-27	Sequence 27, Appl
20	32	100.0	106	4	US-10-389-155-28	Sequence 28, Appl
21	32	100.0	106	4	US-10-325-696-49	Sequence 49, Appl
22	32	100.0	106	4	US-10-325-696-50	Sequence 50, Appl
23	32	100.0	106	4	US-10-325-696-51	Sequence 51, Appl
24	32	100.0	106	4	US-10-389-417-1	Sequence 1, Appli
25	32	100.0	106	4	US-10-389-417-27	Sequence 27, Appl
26	32	100.0	106	4	US-10-389-417-28	Sequence 28, Appl
27	32	100.0	106	4	US-10-452-357-1	Sequence 1, Appli
28	32	100.0	106	4	US-10-452-357-7	Sequence 7, Appli
29	32	100.0	106	4	US-10-452-357-8	Sequence 8, Appli
30	32	100.0	106	4	US-10-452-357-16	Sequence 16, Appl
31	32	100.0	106	5	US-10-717-243-163	Sequence 163, App
32	32	100.0	106	5	US-10-717-243-164	Sequence 164, App
33	32	100.0	106	5	US-10-717-243-165	Sequence 165, App
34	32	100.0	106	6	US-11-133-775-49	Sequence 49, Appl
35	32	100.0	106	6	US-11-133-775-50	Sequence 50, Appl
36	32	100.0	106	6	US-11-133-775-51	Sequence 51, Appl
37	32	100.0	107	5	US-10-661-366-2	Sequence 2, Appli
38	32	100.0	126	4	US-10-389-155-34	Sequence 34, Appl
39	32	100.0	126	4	US-10-389-417-34	Sequence 34, Appl
40	32	100.0	126	4	US-10-452-357-21	Sequence 21, Appl
41	32	100.0	128	4	US-10-244-821-92	Sequence 92, Appl
42	32	100.0	213	5	US-10-822-300-118	Sequence 118, App
43	32	100.0	213	5	US-10-947-432-1	Sequence 1, Appli
44	32	100.0	213	6	US-11-102-621-118	Sequence 118, App
45	32	100.0	215	4	US-10-679-620-120	Sequence 120, App
46	32	100.0	215	6	US-11-132-143-120	Sequence 120, App
47	32	100.0	290	6	US-11-032-773-957	Sequence 957, App
48	32	100.0	319	6	US-11-032-773-955	Sequence 955, App
49	32	100.0	438	4	US-10-244-821-88	Sequence 88, Appl
50	32	100.0	483	4	US-10-679-620-122	Sequence 122, App
51	32	100.0	483	6	US-11-132-143-122	Sequence 122, App
52	32	100.0	498	5	US-10-964-195-13	Sequence 13, Appl
53	32	100.0	506	5	US-10-964-195-11	Sequence 11, Appl
54	32	100.0	510	4	US-10-108-511-5	Sequence 5, Appli
55	32	100.0	510	5	US-10-482-532-5	Sequence 5, Appli
56	30	93.8	503	4	US-10-104-047-3516	Sequence 3516, Ap
57	30	93.8	503	6	US-11-072-512-3516	Sequence 3516, Ap
58	30	93.8	900	4	US-10-408-765A-1339	Sequence 1339, Ap
59	29	90.6	48	4	US-10-424-599-185218	Sequence 185218,
60	29	90.6	168	4	US-10-437-963-113784	Sequence 113784,
61	29	90.6	168	4	US-10-425-115-264904	Sequence 264904,
62	29	90.6	182	4	US-10-425-114-67203	Sequence 67203, A
63	29	90.6	416	4	US-10-767-701-41031	Sequence 41031, A
64	29	90.6	557	5	US-10-739-930-6548	Sequence 6548, Ap

SCORE Search Results Details for Application 10661366 and Search Result us-10-661-366-4.rapbn.

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This page gives you Search Results detail for the Application 10661366 and Search Result us-10-661-366-4.rapbn.

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OM protein - protein search, using sw model

Run on: August 9, 2006, 09:02:15 ; Search time 2.29352 Seconds
(without alignments)
205.442 Million cell updates/sec

Title: US-10-661-366-4
Perfect score: 32
Sequence: 1 TTSNLAS 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 239914 seqs, 67312017 residues

Total number of hits satisfying chosen parameters: 239914

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Published_Applications_AA_New:*
1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
8: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	% Query
--------	------------

No.	Score	Match	Length	DB	ID	Description
1	28	87.5	11	6	US-10-522-086-22	Sequence 22, Appl
2	28	87.5	11	6	US-10-542-682-42	Sequence 42, Appl
3	28	87.5	11	6	US-10-542-682-56	Sequence 56, Appl
4	28	87.5	106	6	US-10-542-682-15	Sequence 15, Appl
5	28	87.5	106	6	US-10-542-682-16	Sequence 16, Appl
6	28	87.5	106	6	US-10-542-682-17	Sequence 17, Appl
7	28	87.5	106	6	US-10-542-682-18	Sequence 18, Appl
8	28	87.5	108	6	US-10-522-086-5	Sequence 5, Appli
9	28	87.5	110	6	US-10-514-516-6	Sequence 6, Appli
10	28	87.5	605	6	US-10-514-516-2	Sequence 2, Appli
11	27	84.4	106	7	US-11-256-060-1	Sequence 1, Appli
12	27	84.4	120	7	US-11-315-067-36	Sequence 36, Appl
13	27	84.4	120	7	US-11-315-067-37	Sequence 37, Appl
14	27	84.4	128	7	US-11-183-218-60	Sequence 60, Appl
15	27	84.4	128	7	US-11-315-067-4	Sequence 4, Appli
16	27	84.4	128	7	US-11-315-067-6	Sequence 6, Appli
17	27	84.4	128	7	US-11-321-444-6	Sequence 6, Appli
18	27	84.4	128	7	US-11-321-444-8	Sequence 8, Appli
19	27	84.4	189	6	US-10-953-349-34528	Sequence 34528, A
20	27	84.4	213	6	US-10-822-231-3	Sequence 3, Appli
21	27	84.4	213	7	US-11-174-287-6	Sequence 6, Appli
22	27	84.4	213	7	US-11-256-060-16	Sequence 16, Appl
23	27	84.4	242	7	US-11-183-325-20	Sequence 20, Appl
24	27	84.4	274	7	US-11-330-403-11560	Sequence 11560, A
25	27	84.4	363	7	US-11-056-355B-42530	Sequence 42530, A
26	27	84.4	376	6	US-10-449-902-44822	Sequence 44822, A
27	27	84.4	382	7	US-11-056-355B-42529	Sequence 42529, A
28	27	84.4	393	7	US-11-056-355B-42528	Sequence 42528, A
29	27	84.4	522	7	US-11-330-403-14671	Sequence 14671, A
30	27	84.4	779	6	US-10-449-902-53491	Sequence 53491, A
31	26	81.2	88	6	US-10-471-571A-3534	Sequence 3534, Ap
32	26	81.2	256	7	US-11-358-419-77	Sequence 77, Appl
33	26	81.2	306	6	US-10-449-902-30402	Sequence 30402, A
34	26	81.2	306	6	US-10-449-902-36762	Sequence 36762, A
35	26	81.2	584	6	US-10-449-902-44384	Sequence 44384, A
36	26	81.2	619	6	US-10-953-349-18449	Sequence 18449, A
37	26	81.2	675	6	US-10-953-349-18448	Sequence 18448, A
38	26	81.2	686	6	US-10-953-349-18447	Sequence 18447, A
39	26	81.2	759	7	US-11-330-403-5806	Sequence 5806, Ap
40	26	81.2	832	6	US-10-953-349-407	Sequence 407, App
41	26	81.2	832	7	US-11-056-355B-24487	Sequence 24487, A
42	26	81.2	832	7	US-11-056-355B-104848	Sequence 104848,
43	26	81.2	832	7	US-11-056-355B-116087	Sequence 116087,
44	26	81.2	984	6	US-10-953-349-406	Sequence 406, App
45	26	81.2	984	7	US-11-056-355B-24486	Sequence 24486, A
46	26	81.2	984	7	US-11-056-355B-104847	Sequence 104847,
47	26	81.2	984	7	US-11-056-355B-116086	Sequence 116086,
48	26	81.2	985	6	US-10-953-349-405	Sequence 405, App
49	26	81.2	985	7	US-11-056-355B-24485	Sequence 24485, A
50	26	81.2	985	7	US-11-056-355B-104846	Sequence 104846,
51	26	81.2	985	7	US-11-056-355B-116085	Sequence 116085,
52	25	78.1	19	7	US-11-134-871-1514	Sequence 1514, Ap
53	25	78.1	130	7	US-11-056-355B-98421	Sequence 98421, A
54	25	78.1	130	7	US-11-056-355B-109660	Sequence 109660,
55	25	78.1	135	7	US-11-056-355B-50185	Sequence 50185, A
56	25	78.1	135	7	US-11-056-355B-98420	Sequence 98420, A
57	25	78.1	135	7	US-11-056-355B-108345	Sequence 108345,
58	25	78.1	135	7	US-11-056-355B-109659	Sequence 109659,
59	25	78.1	135	7	US-11-056-355B-119584	Sequence 119584,

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OM protein - protein search, using sw model

Run on: August 9, 2006, 08:00:49 ; Search time 2.74744 Seconds
(without alignments)
245.144 Million cell updates/sec

Title: US-10-661-366-4
Perfect score: 32
Sequence: 1 TTSNLAS 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : PIR_80:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	32	100.0	86	2 S20651	Ig heavy chain V r
2	29	90.6	534	2 G86385	hypothetical prote
3	29	90.6	546	2 T47018	hypothetical prote
4	29	90.6	546	2 AG0236	probable membrane
5	29	90.6	999	2 F72453	probable cytochrom
6	28	87.5	91	2 S17630	Ig kappa chain V r
7	28	87.5	91	2 S17626	Ig kappa chain V r
8	28	87.5	93	2 S17642	Ig kappa chain V r

9	28	87.5	93	2	S17641	Ig kappa chain V r
10	28	87.5	93	2	S17640	Ig kappa chain V r
11	28	87.5	93	2	S17623	Ig kappa chain V r
12	28	87.5	96	2	C33730	Ig kappa chain V r
13	28	87.5	99	2	PH1059	Ig light chain V r
14	28	87.5	99	2	PH1060	Ig light chain V r
15	28	87.5	99	2	D38601	Ig kappa chain V r
16	28	87.5	99	2	PH1058	Ig light chain V r
17	28	87.5	109	2	PT0404	Ig light chain V r
18	28	87.5	109	2	PT0405	Ig light chain V r
19	28	87.5	130	2	A32513	Ig kappa chain pre
20	28	87.5	140	2	PL0013	Ig kappa chain pre
21	28	87.5	265	2	AH3513	channel protein vi
22	28	87.5	287	2	T31457	protochlorophyllid
23	28	87.5	417	2	D90304	amino acid transpo
24	28	87.5	753	2	S35371	finger protein neu
25	28	87.5	1107	2	S61667	probable membrane
26	28	87.5	1119	2	A88481	protein Cl6A3.6 [i
27	28	87.5	2104	2	T38774	myosin-3 heavy cha
28	28	87.5	2491	2	A57036	talin - slime mold
29	27	84.4	67	2	S24216	Ig kappa chain - m
30	27	84.4	68	2	S26474	Ig kappa chain V r
31	27	84.4	86	2	S20649	Ig heavy chain V r
32	27	84.4	86	2	S26459	Ig kappa chain V r
33	27	84.4	86	2	S29587	Ig kappa chain V r
34	27	84.4	90	2	S26339	Ig kappa chain V r
35	27	84.4	93	2	S17633	Ig kappa chain V r
36	27	84.4	93	2	S17632	Ig kappa chain V r
37	27	84.4	93	2	S17635	Ig kappa chain V r
38	27	84.4	93	2	S17625	Ig kappa chain V r
39	27	84.4	93	2	S17634	Ig kappa chain V r
40	27	84.4	93	2	S17636	Ig kappa chain V r
41	27	84.4	93	2	S17624	Ig kappa chain V r
42	27	84.4	93	2	S17631	Ig kappa chain V r
43	27	84.4	94	2	S26340	Ig light chain V r
44	27	84.4	97	2	PH1085	Ig light chain V r
45	27	84.4	98	2	PH1061	Ig light chain V r
46	27	84.4	101	2	S13696	Ig heavy chain V r
47	27	84.4	102	2	S29582	Ig kappa chain V r
48	27	84.4	102	2	S29584	Ig kappa chain V r
49	27	84.4	102	2	S29588	Ig kappa chain V r
50	27	84.4	102	2	S13697	Ig heavy chain V r
51	27	84.4	103	2	S13695	Ig kappa chain - m
52	27	84.4	103	2	S13698	Ig heavy chain V r
53	27	84.4	104	2	S29592	Ig kappa chain V r
54	27	84.4	104	2	S26475	Ig kappa chain V r
55	27	84.4	105	2	S26338	Ig kappa chain V r
56	27	84.4	106	2	PL0082	Ig kappa chain V r
57	27	84.4	106	2	S29583	Ig kappa chain V r
58	27	84.4	107	2	A42848	Ig light chain V r
59	27	84.4	107	2	S11122	Ig kappa chain V r
60	27	84.4	108	2	S11125	Ig kappa chain V r
61	27	84.4	108	2	PL0278	Ig kappa chain V r
62	27	84.4	108	2	PL0277	Ig kappa chain V r
63	27	84.4	108	2	S38720	Ig light chain V r
64	27	84.4	108	2	PL0276	Ig kappa chain V r
65	27	84.4	108	2	S29581	Ig kappa chain V r
66	27	84.4	108	2	PS0069	Ig kappa chain V r
67	27	84.4	109	2	S13699	Ig kappa chain V r
68	27	84.4	120	2	S66536	Ig light chain V r
69	27	84.4	123	2	S05269	Ig kappa chain pre

SCORE Search Results Details for Application 10661366 and Search Result us-10-661-366-4.rup.

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This page gives you Search Results detail for the Application 10661366 and Search Result us-10-661-366-4.rup.

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OM protein - protein search, using sw model

Run on: August 9, 2006, 07:46:18 ; Search time 21.1672 Seconds
(without alignments)
305.902 Million cell updates/sec

Title: US-10-661-366-4
Perfect score: 32
Sequence: 1 TTSNLAS 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	32	100.0	6680	2 Q5CXT7_CRYPV	Q5cxt7 cryptospori
2	30	93.8	261	2 Q9NXQ0_HUMAN	Q9nxq0 homo sapien
3	30	93.8	554	2 Q2U8A6_ASPOR	Q2u8a6 aspergillus
4	30	93.8	582	2 Q4R338_MACFA	Q4r338 macaca fasc

5	30	93.8	684	2	Q58M11_XENLA	Q58m11 xenopus lae
6	30	93.8	684	2	Q6DCL9_XENLA	Q6dcl9 xenopus lae
7	30	93.8	900	2	Q5T5J6_HUMAN	Q5t5j6 homo sapien
8	30	93.8	900	2	Q8NEK9_HUMAN	Q8nek9 homo sapien
9	30	93.8	900	2	Q9BZQ7_HUMAN	Q9bzq7 homo sapien
10	30	93.8	4315	2	Q6RKJ3_BOTCI	Q6rkj3 botrytis ci
11	29	90.6	137	2	Q6ZLG1_ORYSA	Q6zlg1 oryza sativ
12	29	90.6	175	2	Q81CP3_BACCR	Q81cp3 bacillus ce
13	29	90.6	285	2	Q4L634_STAHJ	Q4l634 staphylococ
14	29	90.6	303	2	Q2XVT0_9CAUD	Q2xvt0 bacterioph
15	29	90.6	303	2	Q3HL44_9CAUD	Q3hl44 bacillus an
16	29	90.6	303	2	Q2LI98_9CAUD	Q2li98 bacillus an
17	29	90.6	303	2	Q2LIF0_9CAUD	Q2lif0 bacillus an
18	29	90.6	303	2	Q3HKY6_9CAUD	Q3hky6 bacillus an
19	29	90.6	303	2	Q2I8C8_9CAUD	Q2i8c8 bacillus an
20	29	90.6	365	2	Q5BWI2_SCHJA	Q5bwi2 schistosoma
21	29	90.6	519	2	Q9NWG4_HUMAN	Q9nwg4 homo sapien
22	29	90.6	532	2	Q9H2U0_HUMAN	Q9h2u0 homo sapien
23	29	90.6	534	2	Q9C6M3_ARATH	Q9c6m3 arabidopsis
24	29	90.6	546	2	Q66B42_YERPS	Q66b42 yersinia ps
25	29	90.6	546	2	Q9ZC50_YERPE	Q9zc50 yersinia pe
26	29	90.6	549	2	Q7QTY6_GIALA	Q7qty6 giardia lam
27	29	90.6	605	2	Q9GM49_MACFA	Q9gm49 macaca fasc
28	29	90.6	623	2	Q5L9H5_BACFN	Q5l9h5 bacteroides
29	29	90.6	686	2	Q9NXF0_HUMAN	Q9nxf0 homo sapien
30	29	90.6	836	2	Q7XY2_ARATH	Q7xyy2 arabidopsis
31	29	90.6	895	2	Q54E19_DICDI	Q54e19 dictyosteli
32	29	90.6	923	2	Q6C314_YARLI	Q6c314 yarrowia li
33	29	90.6	968	2	Q7Z586_HUMAN	Q7z586 homo sapien
34	29	90.6	999	2	Q9Y9L4_AERPE	Q9y9l4 aeropyrum p
35	29	90.6	1332	2	Q86S06_DROME	Q86s06 drosophila
36	29	90.6	1332	2	Q8SZZ7_DROME	Q8szz7 drosophila
37	29	90.6	1343	2	Q9V358_DROME	Q9v358 drosophila
38	29	90.6	1375	2	Q86S05_DROME	Q86s05 drosophila
39	29	90.6	1486	2	Q8TEF1_HUMAN	Q8tef1 homo sapien
40	29	90.6	1491	2	Q9LVQ2_ARATH	Q9lvq2 arabidopsis
41	29	90.6	1541	2	Q7UQJ9_RHOBA	Q7uqj9 rhodopirell
42	29	90.6	2197	2	Q618V1_CAEBR	Q618v1 caenorhabdi
43	29	90.6	2310	2	Q8IBZ1_PLAF7	Q8ibz1 plasmodium
44	29	90.6	2542	2	Q8IWZ3_HUMAN	Q8iwz3 homo sapien
45	29	90.6	2617	2	Q8IWZ2_HUMAN	Q8iwz2 homo sapien
46	29	90.6	2618	2	Q4A5V2_MYCS5	Q4a5v2 mycoplasma
47	29	90.6	4723	2	Q86BA1_DROME	Q86ba1 drosophila
48	29	90.6	4723	2	Q8MUJ8_DROME	Q8muj8 drosophila
49	28	87.5	32	2	Q77UV0_LDV	Q77uv0 lactate deh
50	28	87.5	32	2	Q9YJP6_LDV	Q9yjp6 lactate deh
51	28	87.5	107	2	Q2Z1I3_CALSA	Q2zil3 caldicellul
52	28	87.5	112	2	Q8K1F2_MOUSE	Q8klf2 mus musculu
53	28	87.5	114	2	Q8K1F1_MOUSE	Q8klf1 mus musculu
54	28	87.5	131	2	Q811C3_MOUSE	Q811c3 mus musculu
55	28	87.5	142	2	Q7PC60_MYCSM	Q7pc60 mycobacteri
56	28	87.5	146	2	Q2J8C4_9ACTO	Q2j8c4 frankia sp.
57	28	87.5	160	2	Q72Q84_LEPIC	Q72q84 leptospira
58	28	87.5	160	2	Q8F5X7_LEPIN	Q8f5x7 leptospira
59	28	87.5	207	2	Q9IUQ3_9HIV1	Q9iuq3 human immun
60	28	87.5	213	2	Q5N7E6_ORYSA	Q5n7e6 oryza sativ
61	28	87.5	217	2	Q9IUN8_9HIV1	Q9iun8 human immun
62	28	87.5	221	2	Q8GE29_HELMO	Q8ge29 heliobacill
63	28	87.5	231	2	Q70QD7_9HIV1	Q70qd7 human immun
64	28	87.5	236	2	Q84GE8_CORGL	Q84ge8 corynebacte
65	28	87.5	259	2	Q425X0_DESHA	Q425x0 desulfitoba

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OM protein - protein search, using sw model

Run on: August 9, 2006, 06:40:12 ; Search time 74.3607 Seconds
 (without alignments)
 49.189 Million cell updates/sec

Title: US-10-661-366-5
 Perfect score: 51
 Sequence: 1 HQWSSYPR 8

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 837128

Minimum DB seq length: 0
 Maximum DB seq length: 15

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 500 summaries

Database : A_Geneseq_8:*
 1: geneseqp1980s:*
 2: geneseqp1990s:*
 3: geneseqp2000s:*
 4: geneseqp2001s:*
 5: geneseqp2002s:*
 6: geneseqp2003as:*
 7: geneseqp2003bs:*
 8: geneseqp2004s:*
 9: geneseqp2005s:*
 10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	51	100.0	8	9	ADY75170	Ady75170 Antibody
2	46	90.2	8	2	AAR25957	Aar25957 ICAM-1 in
3	46	90.2	9	8	ADE25810	Ade25810 Anti-alph
4	46	90.2	9	9	AEA44051	Aea44051 Anti-TPO
5	43	84.3	9	8	ADE25811	Ade25811 Anti-alph
6	42	82.4	9	9	AEB70885	Aeb70885 Toll-like
7	42	82.4	14	5	ABG66005	Abg66005 Human ace
8	39	76.5	14	5	ABG66011	Abg66011 Human ace
9	38	74.5	9	3	AAB07959	Aab07959 CDR3 sequ
10	38	74.5	9	8	ADH59663	Adh59663 Light cha
11	38	74.5	9	8	ADH59684	Adh59684 Light cha
12	38	74.5	9	9	AED19123	Aed19123 Oncostati
13	38	74.5	9	10	AEF51135	Aef51135 Variable
14	38	74.5	9	10	AEF76302	Aef76302 Prostate
15	38	74.5	10	5	AAU70357	Aau70357 Mouse Kap
16	37	72.5	9	7	ADJ94572	Adj94572 Humanised
17	37	72.5	14	5	ABG66006	Abg66006 Human ace
18	35	68.6	8	5	ABG66048	Abg66048 Human ace
19	35	68.6	9	5	ABG66039	Abg66039 Human ace
20	35	68.6	10	5	ABG66038	Abg66038 Human ace
21	35	68.6	10	5	ABG66047	Abg66047 Human ace
22	35	68.6	11	5	ABG66037	Abg66037 Human ace
23	35	68.6	11	5	ABG66027	Abg66027 Human ace
24	35	68.6	12	5	ABG66046	Abg66046 Human ace
25	35	68.6	12	5	ABG66036	Abg66036 Human ace
26	35	68.6	12	5	ABG66026	Abg66026 Human ace
27	35	68.6	12	7	ADE15576	Ade15576 Melanoma
28	35	68.6	13	5	ABG66025	Abg66025 Human ace
29	35	68.6	13	5	ABG66035	Abg66035 Human ace
30	35	68.6	14	2	AAW35340	Aaw35340 Human ace
31	35	68.6	14	4	AAU04701	Aau04701 Scrambled
32	35	68.6	14	5	ABG66020	Abg66020 Human ace
33	35	68.6	14	5	ABG65985	Abg65985 Human ace
34	35	68.6	14	5	ABG66008	Abg66008 Human ace
35	35	68.6	14	5	ABG66023	Abg66023 Human ace
36	35	68.6	14	5	ABG65986	Abg65986 Human ace
37	35	68.6	14	5	ABG66021	Abg66021 Human ace
38	35	68.6	14	5	ABG65984	Abg65984 Human ace
39	35	68.6	14	5	ABG66013	Abg66013 Human ace
40	35	68.6	14	5	ABG66022	Abg66022 Human ace
41	35	68.6	14	5	ABG65991	Abg65991 Human ace
42	35	68.6	14	5	ABG65979	Abg65979 Human ace
43	35	68.6	14	5	ABG66012	Abg66012 Human ace
44	35	68.6	14	5	ABG66045	Abg66045 Human ace
45	35	68.6	14	5	ABG65987	Abg65987 Human ace
46	35	68.6	14	5	ABG66003	Abg66003 Human ace
47	35	68.6	14	5	ABG65990	Abg65990 Human ace
48	35	68.6	14	5	ABG66024	Abg66024 Human ace
49	35	68.6	14	9	AEB63852	Aeb63852 Phage dis
50	34	66.7	7	3	AAAY77590	Aay77590 Anti-huma
51	34	66.7	7	4	AAB78859	Aab78859 Anti-huma
52	34	66.7	7	8	ADL11885	Adl11885 CDR-1 lig
53	34	66.7	7	9	ADZ58527	Adz58527 VEGF rece
54	34	66.7	8	6	ADA90369	Ada90369 MS-Roche
55	34	66.7	8	6	ADA89989	Ada89989 Anti-Abet
56	34	66.7	8	6	ADA90368	Ada90368 MS-Roche
57	34	66.7	8	6	ADA90367	Ada90367 MS-Roche

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OM protein - protein search, using sw model

Run on: August 9, 2006, 07:02:53 ; Search time 19.6721 Seconds
(without alignments)
35.596 Million cell updates/sec

Title: US-10-661-366-5
Perfect score: 51
Sequence: 1 HQWSSYPR 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 249102

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Database : Issued Patents_AA:*
1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	38	74.5	9	2	US-09-339-596A-40 Sequence 40, Appl
2	38	74.5	10	2	US-09-563-222C-37 Sequence 37, Appl

3	35	68.6	14	3	US-09-155-076-1	Sequence 1, Appli
4	34	66.7	7	2	US-09-453-718B-20	Sequence 20, Appl
5	32	62.7	9	2	US-09-830-954A-15	Sequence 15, Appl
6	32	62.7	9	2	US-09-830-954A-16	Sequence 16, Appl
7	32	62.7	9	2	US-09-830-954A-17	Sequence 17, Appl
8	32	62.7	9	2	US-09-830-954A-18	Sequence 18, Appl
9	32	62.7	9	2	US-09-830-954A-19	Sequence 19, Appl
10	32	62.7	9	2	US-09-830-954A-20	Sequence 20, Appl
11	31	60.8	9	2	US-08-646-265A-120	Sequence 120, App
12	30	58.8	10	1	US-08-556-597-91	Sequence 91, Appl
13	30	58.8	15	1	US-08-133-271-5	Sequence 5, Appli
14	29	56.9	9	2	US-09-280-028-16	Sequence 16, Appl
15	29	56.9	9	2	US-09-091-071-5	Sequence 5, Appli
16	29	56.9	9	2	US-10-226-795-20	Sequence 20, Appl
17	29	56.9	9	2	US-09-453-718B-14	Sequence 14, Appl
18	29	56.9	9	5	PCT-US94-14106-36	Sequence 36, Appl
19	29	56.9	10	2	US-08-836-561-51	Sequence 51, Appl
20	29	56.9	10	2	US-09-434-122-51	Sequence 51, Appl
21	29	56.9	11	7	5204096-14	Patent No. 5204096
22	29	56.9	11	7	5204096-15	Patent No. 5204096
23	29	56.9	12	2	US-09-563-222C-43	Sequence 43, Appl
24	29	56.9	14	3	US-09-155-076-15	Sequence 15, Appl
25	28	54.9	9	2	US-08-783-853A-14	Sequence 14, Appl
26	28	54.9	9	2	US-09-344-050-14	Sequence 14, Appl
27	28	54.9	9	5	PCT-US93-08435-26	Sequence 26, Appl
28	28	54.9	9	5	PCT-US93-08435-39	Sequence 39, Appl
29	28	54.9	10	1	US-08-602-725-8	Sequence 8, Appli
30	27	52.9	7	2	US-09-281-495-5	Sequence 5, Appli
31	27	52.9	11	7	5270178-10	Patent No. 5270178
32	27	52.9	14	1	US-07-794-288D-174	Sequence 174, App
33	27	52.9	15	1	US-07-794-288D-166	Sequence 166, App
34	27	52.9	15	1	US-07-794-288D-173	Sequence 173, App
35	26	51.0	6	1	US-08-014-979-92	Sequence 92, Appl
36	26	51.0	9	1	US-07-946-421-3	Sequence 3, Appli
37	26	51.0	9	2	US-08-918-148-24	Sequence 24, Appl
38	26	51.0	9	2	US-09-406-535-10	Sequence 10, Appl
39	26	51.0	9	2	US-09-144-280-5	Sequence 5, Appli
40	26	51.0	9	2	US-09-508-413A-12	Sequence 12, Appl
41	26	51.0	9	2	US-09-138-091A-24	Sequence 24, Appl
42	26	51.0	9	2	US-09-644-668A-36	Sequence 36, Appl
43	26	51.0	9	2	US-09-958-620A-10	Sequence 10, Appl
44	26	51.0	10	2	US-09-339-922A-50	Sequence 50, Appl
45	26	51.0	10	2	US-09-016-061-50	Sequence 50, Appl
46	26	51.0	11	1	US-08-482-228-44	Sequence 44, Appl
47	26	51.0	11	2	US-08-482-528-44	Sequence 44, Appl
48	26	51.0	12	1	US-08-811-492-152	Sequence 152, App
49	26	51.0	12	2	US-09-419-381-24	Sequence 24, Appl
50	26	51.0	12	2	US-09-419-381-25	Sequence 25, Appl
51	26	51.0	13	1	US-08-934-222-66	Sequence 66, Appl
52	26	51.0	13	1	US-08-933-402-66	Sequence 66, Appl
53	26	51.0	13	1	US-09-207-621-66	Sequence 66, Appl
54	26	51.0	13	1	US-08-532-818-66	Sequence 66, Appl
55	26	51.0	13	2	US-09-231-797-66	Sequence 66, Appl
56	26	51.0	13	2	US-08-934-224-66	Sequence 66, Appl
57	26	51.0	13	2	US-08-933-843-66	Sequence 66, Appl
58	26	51.0	13	2	US-08-934-223-66	Sequence 66, Appl
59	26	51.0	13	2	US-09-413-492-66	Sequence 66, Appl
60	26	51.0	15	1	US-08-551-128A-1	Sequence 1, Appli
61	26	51.0	15	1	US-08-551-128A-2	Sequence 2, Appli
62	25	49.0	6	1	US-07-801-812A-23	Sequence 23, Appl
63	25	49.0	6	1	US-08-487-568-23	Sequence 23, Appl

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OM protein - protein search, using sw model

Run on: August 9, 2006, 07:35:38 ; Search time 63.6066 Seconds
(without alignments)
58.260 Million cell updates/sec

Title: US-10-661-366-5
Perfect score: 51
Sequence: 1 HQWSSYPR 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 395127

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Database : Published_Applications_AA_Main:*
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4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
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6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
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2	46	90.2	9	5	US-10-507-662-17	Sequence 17, Appl
3	43	84.3	9	5	US-10-507-662-18	Sequence 18, Appl
4	42	82.4	9	6	US-11-009-939-10	Sequence 10, Appl
5	38	74.5	9	4	US-10-461-878-3	Sequence 3, Appli
6	38	74.5	9	5	US-10-461-885-3	Sequence 3, Appli
7	38	74.5	9	5	US-10-986-089A-40	Sequence 40, Appl
8	38	74.5	10	3	US-09-563-222-37	Sequence 37, Appl
9	38	74.5	10	4	US-10-783-950-37	Sequence 37, Appl
10	37	72.5	9	4	US-10-366-709-6	Sequence 6, Appli
11	35	68.6	14	3	US-09-155-076-1	Sequence 1, Appli
12	34	66.7	7	4	US-10-160-232-20	Sequence 20, Appl
13	34	66.7	7	6	US-11-250-411-20	Sequence 20, Appl
14	34	66.7	8	5	US-10-505-313-104	Sequence 104, App
15	32	62.7	9	3	US-09-808-037-15	Sequence 15, Appl
16	32	62.7	9	3	US-09-808-037-16	Sequence 16, Appl
17	32	62.7	9	3	US-09-808-037-17	Sequence 17, Appl
18	32	62.7	9	3	US-09-808-037-18	Sequence 18, Appl
19	32	62.7	9	3	US-09-808-037-19	Sequence 19, Appl
20	32	62.7	9	3	US-09-808-037-20	Sequence 20, Appl
21	32	62.7	9	4	US-10-162-889-15	Sequence 15, Appl
22	32	62.7	9	4	US-10-162-889-16	Sequence 16, Appl
23	32	62.7	9	4	US-10-162-889-17	Sequence 17, Appl
24	32	62.7	9	4	US-10-162-889-18	Sequence 18, Appl
25	32	62.7	9	4	US-10-162-889-19	Sequence 19, Appl
26	32	62.7	9	4	US-10-162-889-20	Sequence 20, Appl
27	32	62.7	9	4	US-10-384-788-15	Sequence 15, Appl
28	32	62.7	9	4	US-10-384-788-16	Sequence 16, Appl
29	32	62.7	9	4	US-10-384-788-17	Sequence 17, Appl
30	32	62.7	9	4	US-10-384-788-18	Sequence 18, Appl
31	32	62.7	9	4	US-10-384-788-19	Sequence 19, Appl
32	32	62.7	9	4	US-10-384-788-20	Sequence 20, Appl
33	32	62.7	9	4	US-10-618-856-15	Sequence 15, Appl
34	32	62.7	9	4	US-10-618-856-16	Sequence 16, Appl
35	32	62.7	9	4	US-10-618-856-17	Sequence 17, Appl
36	32	62.7	9	4	US-10-618-856-18	Sequence 18, Appl
37	32	62.7	9	4	US-10-618-856-19	Sequence 19, Appl
38	32	62.7	9	4	US-10-618-856-20	Sequence 20, Appl
39	32	62.7	9	5	US-10-749-522-15	Sequence 15, Appl
40	32	62.7	9	5	US-10-749-522-16	Sequence 16, Appl
41	32	62.7	9	5	US-10-749-522-17	Sequence 17, Appl
42	32	62.7	9	5	US-10-749-522-18	Sequence 18, Appl
43	32	62.7	9	5	US-10-749-522-19	Sequence 19, Appl
44	32	62.7	9	5	US-10-749-522-20	Sequence 20, Appl
45	32	62.7	9	6	US-11-073-526-15	Sequence 15, Appl
46	32	62.7	9	6	US-11-073-526-16	Sequence 16, Appl
47	32	62.7	9	6	US-11-073-526-17	Sequence 17, Appl
48	32	62.7	9	6	US-11-073-526-18	Sequence 18, Appl
49	32	62.7	9	6	US-11-073-526-19	Sequence 19, Appl
50	32	62.7	9	6	US-11-073-526-20	Sequence 20, Appl
51	32	62.7	13	5	US-10-966-371-17	Sequence 17, Appl
52	31	60.8	8	4	US-10-275-046-42	Sequence 42, Appl
53	31	60.8	9	3	US-09-749-873-120	Sequence 120, App
54	31	60.8	9	4	US-10-344-779-7	Sequence 7, Appli
55	31	60.8	9	4	US-10-738-809-7	Sequence 7, Appli
56	31	60.8	9	5	US-10-769-144-18	Sequence 18, Appl
57	31	60.8	9	5	US-10-903-191-18	Sequence 18, Appl
58	31	60.8	9	5	US-10-839-799-120	Sequence 120, App
59	31	60.8	9	5	US-10-850-635-68	Sequence 68, Appl
60	31	60.8	9	6	US-11-130-206-28	Sequence 28, Appl
61	31	60.8	9	6	US-11-130-206-36	Sequence 36, Appl
62	31	60.8	9	6	US-11-130-206-44	Sequence 44, Appl

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OM protein - protein search, using sw model

Run on: August 9, 2006, 07:36:48 ; Search time 10.0984 Seconds
(without alignments)
53.325 Million cell updates/sec

Title: US-10-661-366-5
Perfect score: 51
Sequence: 1 HQWSSYPR 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 239914 seqs, 67312017 residues

Total number of hits satisfying chosen parameters: 27373

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Database : Published Applications_AA_New:*
1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
8: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
------------	-------	--------------------	----	-------------

1	42	82.4	9	7	US-11-301-373-10	Sequence 10, Appl
2	35	68.6	12	6	US-10-502-771-52	Sequence 52, Appl
3	32	62.7	13	6	US-10-542-516-27	Sequence 27, Appl
4	28	54.9	14	7	US-11-234-731-249	Sequence 249, App
5	27	52.9	9	6	US-10-537-642-821	Sequence 821, App
6	26	51.0	7	6	US-10-499-266-10	Sequence 10, Appl
7	26	51.0	9	7	US-11-219-563-6	Sequence 6, Appli
8	26	51.0	9	7	US-11-219-563-104	Sequence 104, App
9	25	49.0	9	7	US-11-271-008-3	Sequence 3, Appli
10	24	47.1	9	6	US-10-513-148A-10	Sequence 10, Appl
11	24	47.1	9	7	US-11-023-959A-42	Sequence 42, Appl
12	24	47.1	9	7	US-11-263-230-16	Sequence 16, Appl
13	24	47.1	12	6	US-10-511-436A-60	Sequence 60, Appl
14	24	47.1	12	7	US-11-313-152-86	Sequence 86, Appl
15	24	47.1	15	7	US-11-140-487A-2159	Sequence 2159, Ap
16	23	45.1	9	6	US-10-570-220-11	Sequence 11, Appl
17	23	45.1	9	6	US-10-570-220-33	Sequence 33, Appl
18	23	45.1	9	7	US-11-254-182-59	Sequence 59, Appl
19	23	45.1	9	7	US-11-106-762-22	Sequence 22, Appl
20	23	45.1	9	7	US-11-197-665-74	Sequence 74, Appl
21	23	45.1	9	7	US-11-291-698A-46	Sequence 46, Appl
22	23	45.1	12	6	US-10-953-613C-784	Sequence 784, App
23	23	45.1	15	7	US-11-134-871-3281	Sequence 3281, Ap
24	22	43.1	7	6	US-10-542-682-46	Sequence 46, Appl
25	22	43.1	7	6	US-10-542-682-57	Sequence 57, Appl
26	22	43.1	9	6	US-10-953-613C-542	Sequence 542, App
27	22	43.1	9	7	US-11-061-841-223	Sequence 223, App
28	22	43.1	9	7	US-11-324-467-121	Sequence 121, App
29	22	43.1	9	7	US-11-324-634-121	Sequence 121, App
30	22	43.1	12	6	US-10-981-300-60	Sequence 60, Appl
31	22	43.1	12	6	US-10-953-613C-179	Sequence 179, App
32	22	43.1	12	7	US-11-176-182-13	Sequence 13, Appl
33	22	43.1	13	7	US-11-320-412-46	Sequence 46, Appl
34	22	43.1	13	7	US-11-134-871-2533	Sequence 2533, Ap
35	22	43.1	13	7	US-11-134-871-3486	Sequence 3486, Ap
36	22	43.1	15	6	US-10-506-480-15	Sequence 15, Appl
37	22	43.1	15	7	US-11-176-182-49	Sequence 49, Appl
38	21	41.2	5	7	US-11-274-375-60	Sequence 60, Appl
39	21	41.2	7	7	US-11-291-140-23	Sequence 23, Appl
40	21	41.2	7	7	US-11-196-917A-56	Sequence 56, Appl
41	21	41.2	7	7	US-11-196-917A-65	Sequence 65, Appl
42	21	41.2	7	7	US-11-232-404-52	Sequence 52, Appl
43	21	41.2	8	6	US-10-538-066-350	Sequence 350, App
44	21	41.2	9	6	US-10-981-300-44	Sequence 44, Appl
45	21	41.2	9	6	US-10-781-659-39	Sequence 39, Appl
46	21	41.2	9	7	US-11-332-378-71	Sequence 71, Appl
47	21	41.2	9	7	US-11-263-230-6	Sequence 6, Appli
48	21	41.2	10	6	US-10-538-066-351	Sequence 351, App
49	21	41.2	10	6	US-10-538-066-352	Sequence 352, App
50	21	41.2	10	6	US-10-953-613C-210	Sequence 210, App
51	21	41.2	10	6	US-10-513-083A-3	Sequence 3, Appli
52	21	41.2	10	6	US-10-513-083A-4	Sequence 4, Appli
53	21	41.2	10	6	US-10-513-083A-11	Sequence 11, Appl
54	21	41.2	10	6	US-10-781-659-16	Sequence 16, Appl
55	21	41.2	10	6	US-10-781-659-40	Sequence 40, Appl
56	21	41.2	11	7	US-11-196-917A-120	Sequence 120, App
57	21	41.2	11	7	US-11-356-823-3	Sequence 3, Appli
58	21	41.2	12	6	US-10-953-613C-760	Sequence 760, App
59	21	41.2	12	6	US-10-523-277-51	Sequence 51, Appl
60	21	41.2	12	7	US-11-054-072-7500	Sequence 7500, Ap

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OM protein - protein search, using sw model

Run on: August 9, 2006, 06:51:47 ; Search time 11.0164 Seconds
(without alignments)
69.872 Million cell updates/sec

Title: US-10-661-366-5
Perfect score: 51
Sequence: 1 HQWSSYPR 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 2523

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Database : PIR_80:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	32	62.7	12	2 I57678	gene rPLP-A protei
2	25	49.0	10	2 H37196	bradykinin-potenti
3	23	45.1	11	2 I54193	Rhesus blood group
4	23	45.1	13	2 A60379	factor X activator
5	22	43.1	14	2 JH0328	probursin tetradec
6	22	43.1	15	2 PH1366	Ig heavy chain DJ
7	21	41.2	15	2 PA0036	glycine cleavage s
8	20	39.2	10	1 A61126	gonadoliberin - sp

9	20	39.2	10	1	RHAQ2	gonadoliberin II -
10	20	39.2	10	2	B46030	gonadoliberin II -
11	20	39.2	10	2	A59272	peptide-N4-(N-acet
12	20	39.2	10	2	T14212	cytochrome-c oxida
13	20	39.2	15	2	I67525	CD33 antigen homol
14	20	39.2	15	2	S29207	avenin gamma-4 - o
15	19	37.3	8	2	JS0316	leucokinin VI - Ma
16	19	37.3	10	2	A49187	gonadotropin-relea
17	19	37.3	10	2	C41946	T-cell receptor ga
18	18	35.3	10	2	B38887	T-cell receptor ga
19	18	35.3	12	2	S56122	type I DNA methylt
20	18	35.3	12	2	G64003	hypothetical prote
21	18	35.3	13	2	G37266	Ig heavy chain C r
22	18	35.3	13	2	D37267	Ig heavy chain C r
23	18	35.3	13	2	PH0928	T-cell receptor be
24	18	35.3	14	1	BSTD	bombesin - fire-be
25	18	35.3	14	2	B61235	fibroblast-activat
26	18	35.3	15	2	S24159	leukocyte elastase
27	18	35.3	15	2	A49155	vasotocin-associat
28	18	35.3	15	2	B59045	alpha-conotoxin Au
29	18	35.3	15	2	PH1342	Ig heavy chain DJ
30	18	35.3	15	2	C84035	hypothetical prote
31	17	33.3	9	2	S07204	litorin I - Austra
32	17	33.3	10	2	A46030	gonadoliberin I -
33	17	33.3	11	2	PQ0731	unidentified 5.7/3
34	17	33.3	12	2	PH1308	Ig heavy chain DJ
35	17	33.3	13	2	S47358	T-cell antigen rec
36	17	33.3	13	2	S61798	T-cell-specific tr
37	17	33.3	13	2	A60409	bombesin-like pept
38	17	33.3	14	1	LFEBWC	trp operon leader
39	17	33.3	14	1	LFEBWT	trp operon leader
40	17	33.3	15	2	A47628	Fc gamma receptor
41	17	33.3	15	2	PH1365	Ig heavy chain DJ
42	17	33.3	15	2	S33781	acetolactate synth
43	16	31.4	7	2	S36662	dermorphin (Lys-7)
44	16	31.4	8	2	S66646	cardioacceleratory
45	16	31.4	10	2	A60410	beta-neoendorphin
46	16	31.4	10	2	C39191	hypothetical prote
47	16	31.4	11	2	PT0273	Ig heavy chain CRD
48	16	31.4	12	2	PT0274	Ig heavy chain CRD
49	16	31.4	12	2	S29479	hypothetical prote
50	16	31.4	12	2	A61503	sterol carrier pro
51	16	31.4	14	2	H64008	hypothetical prote
52	16	31.4	15	2	PQ0174	stylar glycoprotei
53	16	31.4	15	2	PQ0175	stylar glycoprotei
54	16	31.4	15	2	B56891	gamma 2 gliadin -
55	15	29.4	5	2	E60274	major protein anti
56	15	29.4	5	2	PT0281	Ig heavy chain CRD
57	15	29.4	5	2	PT0308	Ig heavy chain CRD
58	15	29.4	6	2	A31263	dihydrofolate redu
59	15	29.4	6	2	B31263	dihydrofolate redu
60	15	29.4	6	2	PT0618	T-cell receptor be
61	15	29.4	7	2	PC2132	FMRFamide-related
62	15	29.4	8	2	A38887	T-cell receptor ga
63	15	29.4	8	2	A59495	Vesicle associated
64	15	29.4	8	2	A23967	leucopyrokinin - M
65	15	29.4	9	2	S36850	Ig heavy chain V r
66	15	29.4	9	2	A28924	fructose-bisphosph
67	15	29.4	10	1	XAVI6B	angiotensin-conver
68	15	29.4	10	1	RHPGG	gonadoliberin - pi
69	15	29.4	10	1	RHSHG	gonadoliberin - sh

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OM protein - protein search, using sw model

Run on: August 9, 2006, 06:40:52 ; Search time 89.1803 Seconds
(without alignments)
82.979 Million cell updates/sec

Title: US-10-661-366-5
Perfect score: 51
Sequence: .1 HQWSSYPR 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 8966

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Database : UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	32	62.7	12	2	Q80Y04_9MURI	Q80y04 rattus sp.
2	26	51.0	14	2	Q71H36_9HYME	Q71h36 andrena bar
3	25	49.0	10	1	BPP8_BOTIN	P30426 bothrops in
4	25	49.0	13	1	BOML1_BOMVA	P84212 bombina var

5	24	47.1	10	2	Q15342_HUMAN	Q15342	homo sapien
6	24	47.1	11	2	Q6UZ55_9CAEN	Q6uz55	littorina s
7	24	47.1	13	2	Q16392_HUMAN	Q16392	homo sapien
8	23	45.1	13	2	Q7LZ24_VIPAS	Q7lz24	vipera aspi
9	22	43.1	8	2	Q8GTG5_LYCES	Q8gtg5	lycopersico
10	22	43.1	10	1	GON1_CHEPR	P80677	chelyosoma
11	22	43.1	12	2	Q4W371_9LECA	Q4w371	dolichousne
12	22	43.1	14	2	Q7M2Q3_BOVIN	Q7m2q3	bos taurus
13	22	43.1	15	2	Q91PD8_9RHAB	Q91pd8	rabies viru
14	22	43.1	15	2	Q91PE5_9RHAB	Q91pe5	rabies viru
15	22	43.1	15	2	Q91PF4_9RHAB	Q91pf4	rabies viru
16	21.5	42.2	10	2	Q94VD5_VAROL	Q94vd5	varanus oli
17	21.5	42.2	12	2	Q683W7_HUMAN	Q683w7	homo sapien
18	21	41.2	8	2	Q53SB0_HUMAN	Q53sb0	homo sapien
19	21	41.2	8	2	P79940_XENLIA	P79940	xenopus lae
20	21	41.2	10	1	CWP26_LYCES	P80822	lycopersico
21	21	41.2	14	2	Q2MHR3_ECOLI	Q2mhr3	escherichia
22	21	41.2	15	2	Q7MLX0_ARATH	Q7mlx0	arabidopsis
23	21	41.2	15	2	Q9QVF8_9MURI	Q9qvf8	rattus sp.
24	20	39.2	8	2	Q94VA7_9SAUR	Q94va7	varanus sal
25	20	39.2	8	2	Q94VB2_9SAUR	Q94vb2	varanus sal
26	20	39.2	8	2	Q94VB5_9SAUR	Q94vb5	varanus sal
27	20	39.2	9	1	SC40_TITCA	P84683	tityus camb
28	20	39.2	9	2	Q6Xfv2_9PASE	Q6xfv2	nectarinia
29	20	39.2	9	2	Q6Xfw1_9PASE	Q6xfl1	nectarinia
30	20	39.2	9	2	Q94VC6_9SAUR	Q94vc6	varanus pil
31	20	39.2	10	1	GON2_ALLMI	P68073	alligator m
32	20	39.2	10	1	GON2_CHICK	P68072	gallus gall
33	20	39.2	10	1	GON2_CLUPA	P68075	clupea pall
34	20	39.2	10	1	GON2_HYDCO	P68076	hydrolagus
35	20	39.2	10	1	GON2_SQUAC	P68074	squalus aca
36	20	39.2	10	1	SC66_TITCA	P84693	tityus camb
37	20	39.2	10	2	P92762_UROAC	P92762	uromastyx a
38	20	39.2	10	2	Q6Xfw8_9PASE	Q6xfw8	aethopyga b
39	20	39.2	10	2	Q9TFU9_9SAUR	Q9tfu9	teratoscinc
40	20	39.2	12	2	Q2QKX7_9HEMI	Q2qkx7	aphthargeli
41	20	39.2	12	2	Q8CFD7_9MURI	Q8cfd7	rattus sp.
42	20	39.2	13	2	O18890_ATEBE	O18890	ateles belz
43	20	39.2	15	2	Q7M0G8_9MURI	Q7m0g8	mus sp. cd3
44	19	37.3	8	1	LCK4_LEUMA	P21143	leucophaea
45	19	37.3	8	1	LCK6_LEUMA	P19988	leucophaea
46	19	37.3	8	2	O85406_COXBU	O85406	coxiella bu
47	19	37.3	9	1	PVK2_SARBU	P84353	sarcophaga
48	19	37.3	10	1	GON3_PETMA	P30948	petromyzon
49	19	37.3	10	2	Q5SDZ6_9EMBE	Q5sdz6	chlorosping
50	19	37.3	11	1	PVK3_DERVE	P84663	derocalymma
51	19	37.3	11	2	Q4YES8_PLABE	Q4yes8	plasmodium
52	19	37.3	11	2	Q800X7_CHESE	Q800x7	chelydra se
53	19	37.3	12	2	Q5FBL6_9ROSI	Q5fbl6	hibiscus ma
54	19	37.3	12	2	Q5FBL8_9ROSI	Q5fbl8	hibiscus ha
55	19	37.3	12	2	Q5FBP4_9ROSI	Q5fbp4	hibiscus ti
56	19	37.3	12	2	Q5FBR0_9ROSI	Q5fbr0	hibiscus gl
57	19	37.3	13	2	Q6URV3_SORBI	Q6urv3	sorghum bic
58	19	37.3	13	2	Q7TMB4_MOUSE	Q7tmb4	mus musculu
59	19	37.3	13	2	Q9QW04_9MURI	Q9qw04	mus sp. pl
60	19	37.3	14	1	CWP27_TOBAC	P82435	nicotiana t
61	19	37.3	14	1	TAT_HV1Z8	P12511	human immun
62	19	37.3	14	2	Q99902_HUMAN	Q99902	homo sapien
63	19	37.3	14	2	Q2MHS2_RHOCA	Q2mhs2	rhodobacter
64	19	37.3	15	1	CX3B_CONQU	P58842	conus querc
65	19	37.3	15	1	UC14_MAIZE	P80620	zea mays (m

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OM protein - protein search, using sw model

Run on: August 9, 2006, 07:45:18 ; Search time 20.2048 Seconds
(without alignments)
181.033 Million cell updates/sec

Title: US-10-661-366-5
Perfect score: 51
Sequence: 1 HQWSSYPR 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : A_Geneseq_8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	51	100.0	8	9	ADY75170	Ady75170 Antibody
2	51	100.0	107	9	ADY75167	Ady75167 Antibody
3	46	90.2	8	2	AAR25957	Aar25957 ICAM-1 in
4	46	90.2	9	8	ADE25810	Ade25810 Anti-alpha
5	46	90.2	9	9	AEA44051	Aea44051 Anti-TPO
6	46	90.2	100	2	AAR07319	Aar07319 VK domain
7	46	90.2	100	2	AAW14487	Aaw14487 Monoclonal
8	46	90.2	100	2	AAR99876	Aar99876 Monoclonal
9	46	90.2	102	4	AAB62264	Aab62264 Light chain
10	46	90.2	106	8	ADU39964	Adu39964 Antibody
11	46	90.2	106	9	AEB12544	Aeb12544 Antibody
12	46	90.2	106	9	AEB12558	Aeb12558 Humanized
13	46	90.2	108	8	ADE25837	Ade25837 Anti-alpha
14	46	90.2	108	9	AEA89805	Aea89805 Antibody
15	46	90.2	108	9	AEA44098	Aea44098 Anti-TPO
16	46	90.2	110	2	AAR30147	Aar30147 431/26 VK
17	46	90.2	113	4	AAB48936	Aab48936 Anti-TrkA
18	46	90.2	122	2	AAR25958	Aar25958 ICAM-1 in
19	46	90.2	213	2	AAW04301	Aaw04301 Antibody
20	46	90.2	255	8	ADS14282	Ads14282 Murine pr
21	46	90.2	295	4	AAB48934	Aab48934 Anti-TrkA
22	46	90.2	519	8	ADS14288	Ads14288 Murine pr
23	46	90.2	909	2	AAR50092	Aar50092 Humanised
24	43	84.3	9	8	ADE25811	Ade25811 Anti-alpha
25	43	84.3	107	2	AAR88110	Aar88110 Murine an
26	43	84.3	108	8	ADE25838	Ade25838 Anti-alpha
27	43	84.3	129	2	AAR88108	Aar88108 Murine an
28	42	82.4	9	9	AEB70885	Aeb70885 Toll-like
29	42	82.4	14	5	ABG66005	Abg66005 Human ace
30	42	82.4	107	9	AEB70882	Aeb70882 Toll-like
31	42	82.4	108	3	AAV90815	Aay90815 33F8 hybr
32	41	80.4	649	7	ABM85402	Abm85402 Mouse pro
33	40	78.4	475	4	ABG29822	Abg29822 Novel hum
34	40	78.4	838	2	AAW49078	Aaw49078 Solanum t
35	40	78.4	838	9	ADW00956	Adw00956 Amino aci
36	39	76.5	14	5	ABG66011	Abg66011 Human ace
37	39	76.5	100	2	AAW04599	Aaw04599 Anti-DNA
38	39	76.5	100	2	AAW04602	Aaw04602 Anti-DNA
39	39	76.5	108	2	AAW07440	Aaw07440 Anti-DNA
40	39	76.5	298	4	ABG23387	Abg23387 Novel hum
41	39	76.5	302	4	AAB73512	Aab73512 Human tra
42	39	76.5	302	5	ABB97238	Abb97238 Novel hum
43	39	76.5	302	5	ABB07518	Abb07518 Human dru
44	39	76.5	302	6	ADA54657	Ada54657 Human pro
45	39	76.5	316	8	ADR66933	Adr66933 Human pro
46	39	76.5	316	8	ADR66035	Adr66035 Human pro
47	39	76.5	333	7	ADB64622	Adb64622 Human pro
48	39	76.5	585	5	ABB91077	Abb91077 Herbicida
49	39	76.5	2206	7	ABM90427	Abm90427 Rice abio
50	39	76.5	2364	7	ABM88090	Abm88090 Rice abio
51	38	74.5	9	3	AAB07959	Aab07959 CDR3 sequ
52	38	74.5	9	8	ADH59663	Adh59663 Light cha
53	38	74.5	9	8	ADH59684	Adh59684 Light cha
54	38	74.5	9	9	AED19123	Aed19123 Oncostati
55	38	74.5	9	10	AEF51135	Aef51135 Variable
56	38	74.5	9	10	AEF76302	Aef76302 Prostate
57	38	74.5	10	5	AAU70357	Aau70357 Mouse Kap

SCORE Search Results Details for Application 10661366 and Search Result us-10-661-366-5

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OM protein - protein search, using sw model

Run on: August 9, 2006, 08:17:00 ; Search time 5.26962 Seconds
(without alignments)
132.883 Million cell updates/sec

Title: US-10-661-366-5
Perfect score: 51
Sequence: 1 HQWSSYPR 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Issued_Patents_AA:*
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2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	46	90.2	100	1	US-08-308-494A-15	Sequence 15, Appl
2	46	90.2	110	2	US-09-343-698-8	Sequence 8, Appli

3	46	90.2	110	2	US-08-325-955-8	Sequence 8, Appli
4	46	90.2	213	2	US-08-630-820-6	Sequence 6, Appli
5	46	90.2	213	2	US-09-273-453-6	Sequence 6, Appli
6	43	84.3	129	5	PCT-US95-07372-12	Sequence 12, Appl
7	42	82.4	108	2	US-08-483-749A-8	Sequence 8, Appli
8	40	78.4	838	1	US-08-868-786-4	Sequence 4, Appli
9	39	76.5	100	2	US-08-881-037-36	Sequence 36, Appl
10	39	76.5	100	2	US-08-881-037-39	Sequence 39, Appl
11	39	76.5	108	2	US-08-881-037-74	Sequence 74, Appl
12	39	76.5	302	2	US-10-094-749-2225	Sequence 2225, Ap
13	39	76.5	333	2	US-10-104-047-2776	Sequence 2776, Ap
14	38	74.5	9	2	US-09-339-596A-40	Sequence 40, Appl
15	38	74.5	10	2	US-09-563-222C-37	Sequence 37, Appl
16	38	74.5	108	2	US-09-232-290-2	Sequence 2, Appli
17	38	74.5	109	2	US-09-726-219A-268	Sequence 268, App
18	38	74.5	109	2	US-09-196-522-268	Sequence 268, App
19	38	74.5	110	1	US-08-207-996-23	Sequence 23, Appl
20	38	74.5	110	1	US-08-207-996-24	Sequence 24, Appl
21	38	74.5	110	1	US-08-207-996-25	Sequence 25, Appl
22	38	74.5	110	1	US-08-207-996-29	Sequence 29, Appl
23	38	74.5	110	1	US-08-760-840A-23	Sequence 23, Appl
24	38	74.5	110	1	US-08-760-840A-24	Sequence 24, Appl
25	38	74.5	110	1	US-08-760-840A-25	Sequence 25, Appl
26	38	74.5	110	1	US-08-760-840A-30	Sequence 30, Appl
27	38	74.5	110	2	US-09-266-119-23	Sequence 23, Appl
28	38	74.5	110	2	US-09-266-119-24	Sequence 24, Appl
29	38	74.5	110	2	US-09-266-119-25	Sequence 25, Appl
30	38	74.5	110	2	US-09-266-119-30	Sequence 30, Appl
31	38	74.5	110	2	US-09-602-709-23	Sequence 23, Appl
32	38	74.5	110	2	US-09-602-709-24	Sequence 24, Appl
33	38	74.5	110	2	US-09-602-709-25	Sequence 25, Appl
34	38	74.5	110	2	US-09-602-709-30	Sequence 30, Appl
35	38	74.5	128	3	US-09-772-103-6	Sequence 6, Appli
36	38	74.5	128	3	US-09-772-103-8	Sequence 8, Appli
37	38	74.5	130	2	US-09-339-596A-24	Sequence 24, Appl
38	38	74.5	130	2	US-09-339-596A-28	Sequence 28, Appl
39	38	74.5	242	1	US-08-553-497A-26	Sequence 26, Appl
40	38	74.5	242	1	US-08-553-497A-28	Sequence 28, Appl
41	38	74.5	244	1	US-08-553-497A-20	Sequence 20, Appl
42	38	74.5	244	1	US-08-553-497A-22	Sequence 22, Appl
43	38	74.5	246	1	US-08-553-497A-24	Sequence 24, Appl
44	37	72.5	239	2	US-10-092-246-33	Sequence 33, Appl
45	37	72.5	239	2	US-10-096-246A-33	Sequence 33, Appl
46	37	72.5	240	2	US-10-092-246-36	Sequence 36, Appl
47	37	72.5	240	2	US-10-092-246-37	Sequence 37, Appl
48	37	72.5	240	2	US-10-096-246A-34	Sequence 34, Appl
49	37	72.5	240	2	US-10-096-246A-35	Sequence 35, Appl
50	37	72.5	240	2	US-10-096-246A-36	Sequence 36, Appl
51	37	72.5	240	2	US-10-096-246A-37	Sequence 37, Appl
52	37	72.5	278	2	US-09-248-796A-20934	Sequence 20934, A
53	37	72.5	392	2	US-09-583-110-2995	Sequence 2995, Ap
54	37	72.5	403	2	US-09-107-433-2923	Sequence 2923, Ap
55	37	72.5	1070	2	US-09-949-016-11321	Sequence 11321, A
56	36	70.6	258	2	US-09-252-991A-25172	Sequence 25172, A
57	35	68.6	14	3	US-09-155-076-1	Sequence 1, Appli
58	35	68.6	40	1	US-08-370-156-25	Sequence 25, Appl
59	35	68.6	40	2	US-09-310-638-25	Sequence 25, Appl
60	35	68.6	44	3	US-09-155-076-6	Sequence 6, Appli
61	35	68.6	44	3	US-09-155-076-8	Sequence 8, Appli
62	35	68.6	44	3	US-09-155-076-9	Sequence 9, Appli
63	35	68.6	45	1	US-08-370-156-7	Sequence 7, Appli

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OM protein - protein search, using sw model

Run on: August 9, 2006, 09:01:05 ; Search time 17.1195 Seconds
(without alignments)
216.462 Million cell updates/sec

Title: US-10-661-366-5
Perfect score: 51
Sequence: 1 HQWSSYPR 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Published_Applications_AA_Main:*
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4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	51	100.0	8	5	US-10-661-366-5
2	51	100.0	107	5	US-10-661-366-2
3	46	90.2	9	5	US-10-507-662-17

4	46	90.2	106	5	US-10-816-938-25	Sequence 25, Appl
5	46	90.2	108	5	US-10-507-662-44	Sequence 44, Appl
6	46	90.2	213	5	US-10-632-815-6	Sequence 6, Appli
7	43	84.3	9	5	US-10-507-662-18	Sequence 18, Appl
8	43	84.3	108	5	US-10-507-662-45	Sequence 45, Appl
9	43	84.3	108	6	US-11-102-512-53	Sequence 53, Appl
10	42	82.4	9	6	US-11-009-939-10	Sequence 10, Appl
11	42	82.4	96	4	US-10-437-963-112986	Sequence 112986,
12	42	82.4	107	6	US-11-009-939-7	Sequence 7, Appli
13	41	80.4	649	4	US-10-087-192-621	Sequence 621, App
14	40	78.4	475	5	US-10-450-763-60181	Sequence 60181, A
15	40	78.4	838	6	US-11-188-298-15165	Sequence 15165, A
16	39	76.5	223	4	US-10-424-599-163901	Sequence 163901,
17	39	76.5	298	5	US-10-450-763-53746	Sequence 53746, A
18	39	76.5	302	4	US-10-274-694-6	Sequence 6, Appli
19	39	76.5	302	4	US-10-094-749-2225	Sequence 2225, Ap
20	39	76.5	302	5	US-10-332-448-6	Sequence 6, Appli
21	39	76.5	333	4	US-10-104-047-2776	Sequence 2776, Ap
22	39	76.5	333	6	US-11-072-512-2776	Sequence 2776, Ap
23	38	74.5	9	4	US-10-461-878-3	Sequence 3, Appli
24	38	74.5	9	5	US-10-461-885-3	Sequence 3, Appli
25	38	74.5	9	5	US-10-986-089A-40	Sequence 40, Appl
26	38	74.5	10	3	US-09-563-222-37	Sequence 37, Appl
27	38	74.5	10	4	US-10-783-950-37	Sequence 37, Appl
28	38	74.5	93	4	US-10-767-701-41077	Sequence 41077, A
29	38	74.5	107	3	US-09-144-886-75	Sequence 75, Appl
30	38	74.5	107	3	US-09-144-886-78	Sequence 78, Appl
31	38	74.5	107	3	US-09-144-886-90	Sequence 90, Appl
32	38	74.5	107	4	US-10-632-706-72	Sequence 72, Appl
33	38	74.5	107	4	US-10-632-706-75	Sequence 75, Appl
34	38	74.5	108	4	US-10-461-878-9	Sequence 9, Appli
35	38	74.5	108	4	US-10-461-878-14	Sequence 14, Appl
36	38	74.5	108	5	US-10-461-885-9	Sequence 9, Appli
37	38	74.5	108	5	US-10-895-135-47	Sequence 47, Appl
38	38	74.5	108	6	US-11-097-812-39	Sequence 39, Appl
39	38	74.5	109	3	US-09-144-886-79	Sequence 79, Appl
40	38	74.5	109	3	US-09-144-886-91	Sequence 91, Appl
41	38	74.5	109	3	US-09-144-886-96	Sequence 96, Appl
42	38	74.5	109	4	US-10-461-878-12	Sequence 12, Appl
43	38	74.5	109	4	US-10-803-622-268	Sequence 268, App
44	38	74.5	109	4	US-10-803-653-268	Sequence 268, App
45	38	74.5	109	4	US-10-632-706-76	Sequence 76, Appl
46	38	74.5	109	4	US-10-632-706-93	Sequence 93, Appl
47	38	74.5	109	5	US-10-461-885-12	Sequence 12, Appl
48	38	74.5	109	5	US-10-461-885-16	Sequence 16, Appl
49	38	74.5	110	6	US-11-056-776-1	Sequence 1, Appli
50	38	74.5	112	4	US-10-632-706-81	Sequence 81, Appl
51	38	74.5	112	4	US-10-632-706-83	Sequence 83, Appl
52	38	74.5	112	4	US-10-632-706-84	Sequence 84, Appl
53	38	74.5	128	3	US-09-772-103-6	Sequence 6, Appli
54	38	74.5	128	3	US-09-772-103-8	Sequence 8, Appli
55	38	74.5	129	4	US-10-437-963-141584	Sequence 141584,
56	38	74.5	130	5	US-10-986-089A-24	Sequence 24, Appl
57	38	74.5	130	5	US-10-986-089A-28	Sequence 28, Appl
58	38	74.5	146	4	US-10-437-963-168165	Sequence 168165,
59	38	74.5	217	6	US-11-056-776-2	Sequence 2, Appli
60	38	74.5	236	6	US-11-056-776-3	Sequence 3, Appli
61	38	74.5	242	4	US-10-259-087A-20	Sequence 20, Appl
62	38	74.5	242	4	US-10-689-006-20	Sequence 20, Appl
63	38	74.5	364	4	US-10-424-599-265801	Sequence 265801,
64	38	74.5	497	6	US-11-096-568A-28080	Sequence 28080, A

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OM protein - protein search, using sw model

Run on: August 9, 2006, 09:02:15 ; Search time 2.62116 Seconds
(without alignments)
205.442 Million cell updates/sec

Title: US-10-661-366-5
Perfect score: 51
Sequence: 1 HQWSSYPR 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 239914 seqs, 67312017 residues

Total number of hits satisfying chosen parameters: 239914

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

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3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
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1	42	82.4	9	7	US-11-301-373-10	Sequence 10, Appl
2	42	82.4	106	7	US-11-301-373-46	Sequence 46, Appl
3	42	82.4	107	7	US-11-301-373-7	Sequence 7, Appli
4	39	76.5	585	7	US-11-174-307B-204	Sequence 204, App
5	38	74.5	128	7	US-11-321-444-6	Sequence 6, Appli
6	38	74.5	128	7	US-11-321-444-8	Sequence 8, Appli
7	38	74.5	129	7	US-11-330-403-14708	Sequence 14708, A
8	38	74.5	130	6	US-10-449-902-41821	Sequence 41821, A
9	38	74.5	242	7	US-11-183-325-20	Sequence 20, Appl
10	38	74.5	247	6	US-10-953-349-12015	Sequence 12015, A
11	38	74.5	249	6	US-10-953-349-12014	Sequence 12014, A
12	38	74.5	292	6	US-10-953-349-12013	Sequence 12013, A
13	38	74.5	299	7	US-11-330-403-13619	Sequence 13619, A
14	38	74.5	469	7	US-11-330-403-13904	Sequence 13904, A
15	38	74.5	497	7	US-11-056-355B-70243	Sequence 70243, A
16	38	74.5	554	7	US-11-056-355B-70242	Sequence 70242, A
17	38	74.5	561	7	US-11-056-355B-24422	Sequence 24422, A
18	38	74.5	561	7	US-11-056-355B-74755	Sequence 74755, A
19	38	74.5	561	7	US-11-056-355B-75394	Sequence 75394, A
20	38	74.5	579	7	US-11-056-355B-70241	Sequence 70241, A
21	38	74.5	579	7	US-11-330-403-212	Sequence 212, App
22	38	74.5	591	7	US-11-056-355B-24421	Sequence 24421, A
23	38	74.5	591	7	US-11-056-355B-74754	Sequence 74754, A
24	38	74.5	591	7	US-11-056-355B-75393	Sequence 75393, A
25	38	74.5	600	7	US-11-330-403-437	Sequence 437, App
26	38	74.5	600	7	US-11-330-403-6953	Sequence 6953, Ap
27	38	74.5	604	6	US-10-449-902-46102	Sequence 46102, A
28	38	74.5	604	7	US-11-330-403-10796	Sequence 10796, A
29	38	74.5	606	7	US-11-056-355B-24420	Sequence 24420, A
30	38	74.5	606	7	US-11-056-355B-74753	Sequence 74753, A
31	38	74.5	616	7	US-11-330-403-9854	Sequence 9854, Ap
32	38	74.5	624	7	US-11-056-355B-75392	Sequence 75392, A
33	36	70.6	138	7	US-11-330-403-11374	Sequence 11374, A
34	36	70.6	157	6	US-10-449-902-35315	Sequence 35315, A
35	36	70.6	167	6	US-10-449-902-51176	Sequence 51176, A
36	36	70.6	183	6	US-10-449-902-29192	Sequence 29192, A
37	36	70.6	183	6	US-10-449-902-30835	Sequence 30835, A
38	36	70.6	1202	7	US-11-056-355B-75882	Sequence 75882, A
39	36	70.6	1257	7	US-11-056-355B-75881	Sequence 75881, A
40	36	70.6	1295	7	US-11-056-355B-75880	Sequence 75880, A
41	35	68.6	12	6	US-10-502-771-52	Sequence 52, Appl
42	35	68.6	27	7	US-11-352-073-3	Sequence 3, Appli
43	35	68.6	40	7	US-11-352-073-2	Sequence 2, Appli
44	35	68.6	171	6	US-10-953-349-6739	Sequence 6739, Ap
45	35	68.6	219	6	US-10-953-349-6738	Sequence 6738, Ap
46	35	68.6	322	6	US-10-953-349-6737	Sequence 6737, Ap
47	35	68.6	394	6	US-10-471-571A-3384	Sequence 3384, Ap
48	35	68.6	509	7	US-11-056-355B-76966	Sequence 76966, A
49	35	68.6	512	7	US-11-056-355B-106720	Sequence 106720,
50	35	68.6	512	7	US-11-056-355B-117959	Sequence 117959,
51	35	68.6	529	7	US-11-056-355B-76965	Sequence 76965, A
52	35	68.6	529	7	US-11-056-355B-106719	Sequence 106719,
53	35	68.6	529	7	US-11-056-355B-117958	Sequence 117958,
54	34	66.7	196	6	US-10-953-349-23794	Sequence 23794, A
55	34	66.7	215	6	US-10-953-349-11020	Sequence 11020, A
56	34	66.7	216	6	US-10-953-349-23793	Sequence 23793, A
57	34	66.7	242	6	US-10-953-349-11018	Sequence 11018, A
58	34	66.7	321	6	US-10-953-349-23062	Sequence 23062, A
59	34	66.7	369	6	US-10-953-349-23061	Sequence 23061, A
60	34	66.7	389	6	US-10-953-349-13621	Sequence 13621, A

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A;Cross-references: UNIPROT:O53916; UNIPARC:UPI00000D3B02; GB:AL022002; GB:AL123456; HQWSSYP 8 |||: || Db 95 HQWAGNPR 102 RESULT 29 S76039 probable dihydroorotate oxidase (I Hosouchi, T.; Matsuno, A.; Muraki, A.; Nakazaki, N.; Naruo, K.; Okumura, S.; Shimpou, S.; Takeuchi, A.; Molecule type: DNA A;Residues: 1-87 A;Cross-references: UNIPROT:P74782; UNIPARC:UPI0000 EMBL Data Library, June 1996 C;Genetics: A;Gene: pyrD C;Superfamily: dihydroorotate oxidase C; C;Accession: G89822 R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cmeticillin-resistant *Staphylococcus aureus*. A;Reference number: A89758; MUID:21311952; PMID:1 Mismatches 2; Indels 0; Gaps 0; Qy 1 HQWSSYP 7 | || || Db 163 HLWSGY 169 RESULT 31 T3475 A;Residues: 1-420 A;Cross-references: UNIPROT:O86565; UNIPARC:UPI000012B87C; EMBL:AL03: hydroxymethyltransferase (EC 2.1.2.1) glyA2 - *Mycobacterium tuberculosis* (strain H37RV) C;Spec J.; Moule, S.; Murphy, L.; Oliver, S.; Osborne, J.; Quail, M.A.; Rajandream, M.A.; Rogers, J.; Rutte A;Cross-references: UNIPROT:O53615; UNIPARC:UPI000012B4E6; GB:AL021428; GB:AL123456; I Conservative 1; Mismatches 0; Indels 0; Gaps 0; Qy 3 WSSYP 8 ||:||| Db 175 WSAYPR 180 RESL Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd, S.; Hornsby, T.; Jagels, K.; Lacroix, C.; Maclean, J.; M DNA A;Residues: 1-426 A;Cross-references: UNIPROT:Q9X794; UNIPARC:UPI000012B870; GB:AL: H37RV) N;Alternate names: serine hydroxymethyltransferase C;Species: *Mycobacterium tuberculo*: Oliver, S.; Osborne, J.; Quail, M.A.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, A;Cross-references: UNIPROT:O53441; UNIPARC:UPI00001135C7; GB:AL021897; GB:AL123456; I Conservative 1; Mismatches 0; Indels 0; Gaps 0; Qy 3 WSSYP 8 ||:||| Db 172 WSAYPR 177 RESL Mewes, H.W.; Rudd, S.; Lemcke, K.; Mayer, K.F.X. submitted to the Protein Sequence Database, M 475/Domain: cytochrome P450 homology F;453/Binding site: heme iron (Cys) (axial ligand) #statu C;Accession: F96741 R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Kim, C.J.; Koo, H.L.; Kremenetskaia, I.; Kurtz, D.B.; Kwan, A.; Lam, B.; Langin-Hooper, S.; Lee, A Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A;Title: Sequence and analysis of chromosc DB 2; Length 512; Best Local Similarity 83.3%; Pred. No. 1.2e+02; Matches 5; Conservative 1; Mi Jablonski, L.; Larsen, N.; D'Souza, M.; Bernal, A.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; PID:g17983469; GSPDB:GN00190 A;Experimental source: strain 16M C;Genetics: A;Gene: BME11: magnesium (His) (shared with chain II) #status predicted F;414/Binding site: heme a3 iron (His) (#text_change 09-Jul-2004 C;Accession: AB2671 R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D. M.; Krespan, W.; Perry, M.; Gordon-Kamm, B.; Liao, L.; Kim, S.; Hendrick, C.; Zhao, Z.; Dolan, M. source: strain C58 (Dupont) C;Genetics: A;Gene: coxA A;Map position: circular chromosome C;Su #status predicted F;434/Binding site: heme a3 iron (His) (axial ligand) #status predicted Query M: Chapman, T.C.; Christner, C.E.; Deal, C.D.; de la Hoz, D.M.; Gentry, M.K.; Ogert, R.A.; Rush, R.S. J.D.; Rosenberry, T.L. J. Biol. Chem. 266, 7481-7487, 1991 A;Title: Bovine brain acetylcholinester: UNIPARC:UPI00001758E1; UNIPARC:UPI00001758E2; UNIPARC:UPI00001758E3; UNIPARC:UPI00 bovine acetylcholinesterase. A;Reference number: A91370; MUID:87080761; PMID:3792544 A;Ac 35; DB 2; Length 583; Best Local Similarity 83.3%; Pred. No. 1.4e+02; Matches 5; Conservative 1 adult rabbit tissues and during development. A;Reference number: S48724; MUID:95010096; PMII 559 HRWSSY 564 RESULT 41 ACRYE acetylcholinesterase (EC 3.1.1.7) precursor, 11S form [valida: structure of *Torpedo californica* acetylcholinesterase deduced from its cDNA sequence. A;Reference K.; Taylor, S.S.; Friedmann, T.; Taylor, P. Fed. Proc. 45, 2976-2981, 1986 A;Title: Primary structu acetylcholinesterase. A;Reference number: A92701; MUID:89066695; PMID:3198606 A;Accession: Chem. 260, 12185-12189, 1985 A;Title: Primary structures of the catalytic subunits from two mole acetylcholinesterase from *Torpedo* and from cobra venom. A;Reference number: A41117; MUID:91 PS0113; MUID:90166618; PMID:2306366 A;Accession: S15677 A;Status: preliminary A;Molecule 1 1991 A;Reference number: A50061; PDB:1ACE A;Contents: annotation; X-ray crystallography, 2.8

5.6S form C;Comment: Synapses usually contain this 11S (asymmetric) form of cholinesterase with cholinesterase; cholinesterase homology C;Keywords: alternative splicing; carboxylic ester hydrolase F;221/Active site: Ser #status experimental F;348,461/Active site: Glu, His #status predicted F;43 electric ray) C;Date: 23-Apr-1993 #sequence_revision 15-Nov-1996 #text_change 09-Jul-2004 C; acetylcholinesterase: primary structure of the precursor of a catalytic subunit; existence of multiple acetylcholinesterase transcripts in Torpedo electric organ; primary structure of the precursor of the of low-salt-soluble and detergent-soluble amphiphilic dimers of Torpedo acetylcholinesterase. Comp splicing; carboxylic ester hydrolase; glycoprotein; neurotransmitter degradation; synapse F;1-24/C Similarity 83.3%; Pred. No. 1.4e+02; Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0; U.S.A. 87, 9688-9692, 1990 A;Title: Molecular cloning and construction of the coding region for human alternative splicing should occur in the region 5' to ABGACHE so this sequence should represent an 415,'Y',417,'X',419;'X',421-422;'XX',467-468,'DV',471-472,'X',474-477,'X',479-480;'X',529-530,'Y' C;Keywords: alternative splicing; carboxylic ester hydrolase; glycoprotein; phosphatidylinositol link C;Accession: JH0314 R;Rachinsky, T.L.; Camp, S.; Li, Y.; Ekstroem, T.J.; Newton, M.; Taylor, P. N. cholinesterase homology C;Keywords: carboxylic ester hydrolase; glycoprotein; membrane protein Similarity 83.3%; Pred. No. 1.4e+02; Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0; multiple molecular forms and complementarity with a Torpedo collagenic subunit. A;Reference number hydrolase; glycoprotein; membrane protein; muscle; nerve; neurotransmitter degradation; synapse 1.4e+02; Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0; Qy 1 HQWSSY 6 |:|||| Db 5 PMID:8049273 A;Accession: S47639 A;Molecule type: mRNA A;Residues: 1-767 A;Cross-reference Pyrococcus kodakaraensis C;Species: Pyrococcus kodakaraensis C;Date: 21-Jan-2000 #sequence_ translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-1215 A;Cross-references: UN Mar-1990 #sequence_revision 09-Mar-1990 #text_change 21-Jan-2000 C;Accession: D33730 R;La UNIPARC:UPI00001767EE C;Superfamily: immunoglobulin V region; immunoglobulin homology C;I #text_change 09-Jul-2004 C;Accession: A01943 R;Kwan, S.P.; Max, E.E.; Seidman, J.G.; Leder, P protein, in which there is a deletion of two amino acids at the V-J recombination site (after position immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer F;1-22/Domain: pernix (strain K1) C;Species: Aeropyrum pernix C;Date: 20-Aug-1999 #sequence_revision 20-Aug 1999 A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr 83.3%; Pred. No. 48; Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0; Qy 3 WSSYPR { S12097; MUID:91045080; PMID:2235496 A;Accession: S12097 A;Status: preliminary A;Molecule 1 Chlamydophila pneumoniae, Chlamydia pneumoniae C;Date: 02-Mar-2001 #sequence_revision 02- 195 A;Cross-references: UNIPROT:Q9Z8B8; UNIPARC:UPI00000D41BE; GB:BA000008; NID:g8978 pneumoniae (strains CWL029 and AR39) N;Alternate names: ct276 hypothetical protein C;Species: A;Accession: C72081 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-195 A;Cross-refer Salzberg, S.L.; Eisen, J.; Fraser, C.M. Nucleic Acids Res. 28, 1397-1406, 2000 A;Title: Genome seq CPn0425; CP0328 C;Superfamily: conserved hypothetical protein TC0548 Query Match 66.7%; Scd 1986 A;Title: Isolation of a novel prolactin-like cDNA clone from developing rat placenta. A;Referer 83.3%; Pred. No. 82; Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0; Qy 1 HQWSSY number: S47351 A;Accession: S47352 A;Status: preliminary A;Molecule type: mRNA A;Residues: C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004 C;Accession: F references: UNIPROT:Q98PQ7; UNIPARC:UPI00000C80E8; GB:AL445566; PID:g14090077; PIDN:C 1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004 C;Accession: S47351 R;Keiper, DB 2; Length 237; Best Local Similarity 83.3%; Pred. No. 85; Matches 5; Conservative 0; Mismatch Chillingworth, T.; Connor, R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, PMID:11234002 A;Accession: C87192 A;Status: preliminary A;Molecule type: DNA A;Residues: 1- T41335 hypothetical protein SPCC364.01 - fission yeast (Schizosaccharomyces pombe) C;Species: UNIPARC:UPI0000069F29; EMBL:AL022243; PIDN:CAA18283.1; GSPDB:GN00067; SPDB:SPCC364 glucosyltransferase I (EC 2.4.1.58) - Salmonella enterica subsp. enterica serovar Typhi (strain CT1 Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, J.; Feltwell, T.; Hamlin, N.; Haque, A.; Hien, type: DNA A;Residues: 1-336 A;Cross-references: UNIPARC:UPI000005A6FB; GB:AL513382; PIDN galactosyltransferase (EC 2.4.1.44) - Salmonella enterica subsp. enterica serovar Typhi (strain CT1 A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, J.; Feltwell, T.; Hamlin, N.; Haque, A.; Hie A;Molecule type: DNA A;Residues: 1-337 A;Cross-references: UNIPARC:UPI000005A6FA; GB:AL51 protein APE2382 - Aeropyrum pernix (strain K1) C;Species: Aeropyrum pernix C;Date: 20-Aug-199

SCORE Search Results Details for Application 10661366 and Search Result us-10-661-366-5.rup.

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OM protein - protein search, using sw model

Run on: August 9, 2006, 07:46:18 ; Search time 24.1911 Seconds
(without alignments)
305.902 Million cell updates/sec

Title: US-10-661-366-5
Perfect score: 51
Sequence: 1 HQWSSYPR 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	41	80.4	235	2 Q73SV8_MYCPA	Q73sv8 mycobacteri
2	41	80.4	936	2 Q99NI3_MOUSE	Q99ni3 mus musculu
3	40	78.4	258	2 Q6G4I1_BARHE	Q6g4i1 bartonella
4	40	78.4	379	2 Q7T3S5_BRARE	Q7t3s5 brachydanio

5	40	78.4	838	1	PHSH_SOLTU	P32811	solanum tub
6	39	76.5	258	2	Q2QXR4_ORYSA	Q2qxr4	oryza sativ
7	39	76.5	302	2	Q969I3_HUMAN	Q969i3	homo sapien
8	39	76.5	333	2	Q8NAW8_HUMAN	Q8naw8	homo sapien
9	39	76.5	392	2	Q9LMW9_ARATH	Q9lmw9	arabidopsis
10	39	76.5	422	2	Q9LM89_ARATH	Q9lm89	arabidopsis
11	39	76.5	1451	2	Q67WN2_ORYSA	Q67wn2	oryza sativ
12	38	74.5	108	1	KV6K_MOUSE	P04945	mus musculu
13	38	74.5	244	2	Q67Y79_ARATH	Q67y79	arabidopsis
14	38	74.5	264	2	Q3SH96_THIDA	Q3sh96	thiobacillu
15	38	74.5	285	2	Q4P289_USTMA	Q4p289	ustilago ma
16	38	74.5	363	2	Q2NRB5_SODGL	Q2nrb5	sodalis glo
17	38	74.5	411	2	Q9N5J2_CAEEL	Q9n5j2	caenorhabdi
18	38	74.5	430	2	Q6N9Z9_RHOPA	Q6n9z9	rhodopseudo
19	38	74.5	471	2	Q665Z4_YERPS	Q665z4	yersinia ps
20	38	74.5	591	2	Q3ECP0_ARATH	Q3ecp0	arabidopsis
21	38	74.5	604	2	Q6ZC85_ORYSA	Q6zc85	oryza sativ
22	38	74.5	605	2	Q40VQ8_KINRA	Q40vq8	kineococcus
23	38	74.5	904	2	Q4DQJ9_TRYCR	Q4dqj9	trypanosoma
24	38	74.5	920	2	Q4CZJ4_TRYCR	Q4czj4	trypanosoma
25	37	72.5	117	2	Q3SML2_THIDA	Q3sml2	thiobacillu
26	37	72.5	143	2	Q6H6H2_ORYSA	Q6h6h2	oryza sativ
27	37	72.5	242	2	Q59TF2_CANAL	Q59tf2	candida alb
28	37	72.5	320	2	Q3VAF4_9SPHN	Q3vaf4	sphingopyxi
29	37	72.5	322	2	Q3WTS4_9RHIZ	Q3wts4	mesorhizobi
30	37	72.5	335	2	Q9ZIT4_ECOLI	Q9zit4	escherichia
31	37	72.5	338	2	Q329M8_SHIDS	Q329m8	shigella dy
32	37	72.5	340	2	Q98L20_RHILO	Q98l20	rhizobium l
33	37	72.5	380	2	Q3VMQ0_9CHLB	Q3vmq0	pelodictyon
34	37	72.5	386	2	Q49ZK2_STAS1	Q49zk2	staphylococ
35	37	72.5	387	2	Q3CHR9_THEET	Q3chr9	thermoanaer
36	37	72.5	388	1	GAL1_STACA	Q9rgs1	staphylococ
37	37	72.5	388	1	GAL1_STRTR	Q9zb10	streptococc
38	37	72.5	388	2	Q64FU6_STRTR	Q64fu6	streptococc
39	37	72.5	388	2	Q64FV1_STRTR	Q64fv1	streptococc
40	37	72.5	388	2	Q64FV5_STRTR	Q64fv5	streptococc
41	37	72.5	388	2	Q8VS93_STRSL	Q8vs93	streptococc
42	37	72.5	388	2	Q8VS87_STRTR	Q8vs87	streptococc
43	37	72.5	388	2	Q38XL2_LACSS	Q38xl2	lactobacill
44	37	72.5	388	2	Q5LYY7_STRT1	Q5lyy7	streptococc
45	37	72.5	388	2	Q5M3K0_STRT2	Q5m3k0	streptococc
46	37	72.5	389	2	Q2WV67_CLOBE	Q2wv67	clostridium
47	37	72.5	390	1	GAL1_THETN	Q8r8r7	thermoanaer
48	37	72.5	392	1	GAL1_STRPN	Q97nz6	streptococc
49	37	72.5	392	1	GAL1_STRR6	Q8dnk7	streptococc
50	37	72.5	392	2	Q840N8_STRGN	Q840n8	streptococc
51	37	72.5	632	2	Q4P6E5_USTMA	Q4p6e5	ustilago ma
52	37	72.5	896	2	Q6C160_YARLI	Q6c160	yarrowia li
53	37	72.5	919	2	Q5RCB5_PONPY	Q5rcb5	pongo pygma
54	37	72.5	961	2	Q4JLV4_CRIGR	Q4jlv4	cricetulus
55	37	72.5	1046	2	Q5F3P4_CHICK	Q5f3p4	gallus gall
56	37	72.5	1064	1	PK3CB_MOUSE	Q8bti9	mus musculu
57	37	72.5	1064	2	Q3U4Q1_MOUSE	Q3u4q1	mus musculu
58	37	72.5	1066	2	Q5F4A2_CHICK	Q5f4a2	gallus gall
59	37	72.5	1070	1	PK3CB_HUMAN	P42338	homo sapien
60	37	72.5	1070	1	PK3CB_RAT	Q9z110	rattus norv
61	37	72.5	1378	2	Q38FP7_9TRYP	Q38fp7	trypanosoma
62	36	70.6	112	2	Q4IW33_AZOVI	Q4iw33	azotobacter
63	36	70.6	123	2	Q9NXN7_HUMAN	Q9nxn7	homo sapien
64	36	70.6	135	2	Q8GRY0_ORYSA	Q8gry0	oryza sativ
65	36	70.6	138	2	Q7XKD6_ORYSA	Q7xkd6	oryza sativ

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OM protein - protein search, using sw model

Run on: August 9, 2006, 06:40:12 ; Search time 92.9508 Seconds
(without alignments)
49.189 Million cell updates/sec

Title: US-10-661-366-6
Perfect score: 54
Sequence: 1 GYTFTSQDIN 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 837128

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Database : A_Geneseq_8:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*
- 9: geneseqp2005s:*
- 10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	54	100.0	10	9	ADY75171	Ady75171 Antibody
2	48	88.9	10	8	ADP47210	Adp47210 Human pho
3	40	74.1	10	3	AAy78322	Aay78322 Anti-zeta
4	40	74.1	10	8	ADO60470	Ado60470 Mouse ant
5	40	74.1	10	9	AEB24622	Aeb24622 Humanized
6	38	70.4	10	8	ADQ90710	Adq90710 Anti-VEGF
7	36	66.7	10	9	AEC22286	Aec22286 VH domain
8	36	66.7	10	10	AEG03109	Aeg03109 CD200-spe
9	36	66.7	11	10	AEE03770	Aee03770 Antibody
10	35	64.8	10	2	AAW70611	Aaw70611 Anti-VEGF
11	35	64.8	10	5	AAU72831	Aau72831 Anti-NKG2
12	35	64.8	10	5	AAG80311	Aag80311 Anti-huma
13	35	64.8	10	5	ABP61180	Abp61180 Humanised
14	35	64.8	10	8	ADQ90711	Adq90711 Anti-VEGF
15	35	64.8	10	8	ADP79603	Adp79603 Murine 2H
16	35	64.8	10	8	ADR89785	Adr89785 Anti-CD70
17	35	64.8	10	8	ADU80233	Adu80233 CD20 bind
18	35	64.8	10	9	ADW21312	Adw21312 Mouse ant
19	35	64.8	10	9	ADW86100	Adw86100 Mouse DS6
20	35	64.8	10	9	AEA40554	Aea40554 Anti-VEGF
21	35	64.8	10	9	AEA40550	Aea40550 Anti-VEGF
22	35	64.8	10	9	AEB23187	Aeb23187 Anti-trkC
23	35	64.8	10	9	AEE18940	Aee18940 Murine an
24	35	64.8	10	10	AEE26269	Aee26269 Humanized
25	35	64.8	10	10	AEE64972	Aee64972 Humanised
26	35	64.8	10	10	AEE10474	Aeel0474 Murine 2H
27	35	64.8	10	10	AEF64237	Aef64237 Humanized
28	35	64.8	10	10	AEG04993	Aeg04993 Anti-CD20
29	35	64.8	13	5	ADG67307	Adg67307 Human ant
30	35	64.8	13	5	ADG67306	Adg67306 Human ant
31	35	64.8	13	8	ADS19052	Ads19052 Human A5
32	34	63.0	10	8	ADO32142	Ado32142 Mouse ant
33	34	63.0	10	8	ADS94322	Ads94322 Antibody
34	34	63.0	10	9	ADV86680	Adv86680 Anti-FLJ3
35	34	63.0	10	9	AEA40568	Aea40568 Anti-VEGF
36	33	61.1	8	8	ADL27410	Adl27410 Amino aci
37	33	61.1	10	8	ADE85702	Ade85702 Human Eph
38	33	61.1	10	8	ADH17813	Adh17813 AbM softw
39	33	61.1	10	9	ADW11444	Adw11444 Murine an
40	33	61.1	10	9	ADY32282	Ady32282 Human Eph
41	33	61.1	10	9	AEB17138	Aeb17138 EphA2-spe
42	33	61.1	10	9	AEA42938	Aea42938 EphA2 ant
43	33	61.1	10	9	AEB23205	Aeb23205 Mouse ant
44	33	61.1	10	9	AEB23199	Aeb23199 Anti-trkC
45	33	61.1	10	9	AEC05617	Aec05617 Murine EM
46	33	61.1	10	9	AED65290	Aed65290 Murine an
47	33	61.1	10	10	AEF68864	Aef68864 Mouse ant
48	33	61.1	10	10	AEF68760	Aef68760 Anti c-me
49	33	61.1	10	10	AEF68678	Aef68678 Anti c-me
50	33	61.1	10	10	AEF68813	Aef68813 Anti c-me
51	33	61.1	10	10	AEF68768	Aef68768 Anti c-me
52	33	61.1	10	10	AEF68751	Aef68751 Anti c-me
53	33	61.1	10	10	AEF68752	Aef68752 Anti c-me
54	33	61.1	10	10	AEF76318	Aef76318 Prostate
55	33	61.1	10	10	AEG03073	Aeg03073 CD200-spe
56	33	61.1	10	10	AEG03103	Aeg03103 CD200-spe
57	33	61.1	10	10	AEG02784	Aeg02784 Anti-ghre

SCORE Search Results Details for Application 10661366 and Search Result us-10-661-366-6.closed.ra1.

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OM protein - protein search, using sw model

Run on: August 9, 2006, 07:02:53 ; Search time 24.5902 Seconds
(without alignments)
35.596 Million cell updates/sec

Title: US-10-661-366-6
Perfect score: 54
Sequence: 1 GYTFTSQDIN 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 249102

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Database : Issued_Patents_AA:*
1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					
No.	Score	Match	Length	ID		Description

1	35	64.8	10	2	US-08-908-469-1	Sequence 1, Appli
2	32	59.3	10	2	US-09-339-922A-34	Sequence 34, Appl
3	32	59.3	10	2	US-09-016-061-34	Sequence 34, Appl
4	32	59.3	10	2	US-09-440-781-19	Sequence 19, Appl
5	30	55.6	10	2	US-09-339-922A-52	Sequence 52, Appl
6	30	55.6	10	2	US-09-016-061-52	Sequence 52, Appl
7	29	53.7	10	2	US-09-440-781-20	Sequence 20, Appl
8	29	53.7	10	2	US-08-908-469-130	Sequence 130, App
9	28	51.9	10	2	US-08-974-899-10	Sequence 10, Appl
10	28	51.9	10	2	US-09-795-798-10	Sequence 10, Appl
11	27	50.0	6	2	US-09-556-605-52	Sequence 52, Appl
12	27	50.0	7	2	US-09-556-605-51	Sequence 51, Appl
13	27	50.0	8	2	US-09-556-605-50	Sequence 50, Appl
14	27	50.0	9	2	US-09-556-605-49	Sequence 49, Appl
15	27	50.0	10	2	US-09-556-605-48	Sequence 48, Appl
16	27	50.0	10	2	US-09-339-922A-48	Sequence 48, Appl
17	27	50.0	10	2	US-09-339-922A-50	Sequence 50, Appl
18	27	50.0	10	2	US-09-016-061-48	Sequence 48, Appl
19	27	50.0	10	2	US-09-016-061-50	Sequence 50, Appl
20	27	50.0	10	2	US-09-440-781-21	Sequence 21, Appl
21	27	50.0	10	2	US-08-908-469-86	Sequence 86, Appl
22	27	50.0	10	2	US-08-908-469-88	Sequence 88, Appl
23	27	50.0	10	2	US-08-908-469-128	Sequence 128, App
24	27	50.0	11	2	US-09-556-605-47	Sequence 47, Appl
25	27	50.0	12	2	US-09-556-605-46	Sequence 46, Appl
26	27	50.0	13	2	US-09-556-605-45	Sequence 45, Appl
27	27	50.0	14	2	US-09-556-605-44	Sequence 44, Appl
28	27	50.0	15	2	US-09-556-605-43	Sequence 43, Appl
29	26	48.1	9	2	US-09-534-717-323	Sequence 323, App
30	26	48.1	10	2	US-09-786-066-11	Sequence 11, Appl
31	26	48.1	10	2	US-10-122-675-23	Sequence 23, Appl
32	26	48.1	10	2	US-10-850-055-39	Sequence 39, Appl
33	26	48.1	10	2	US-10-850-055-40	Sequence 40, Appl
34	26	48.1	10	2	US-10-850-055-41	Sequence 41, Appl
35	26	48.1	10	2	US-10-850-055-42	Sequence 42, Appl
36	26	48.1	11	1	US-08-621-803-99	Sequence 99, Appl
37	26	48.1	11	2	US-09-217-352-99	Sequence 99, Appl
38	26	48.1	11	2	US-10-850-055-38	Sequence 38, Appl
39	26	48.1	12	1	US-08-811-492-153	Sequence 153, App
40	26	48.1	15	2	US-10-850-055-37	Sequence 37, Appl
41	26	48.1	15	3	US-09-423-351C-11	Sequence 11, Appl
42	26	48.1	15	3	US-09-423-351C-12	Sequence 12, Appl
43	26	48.1	15	3	US-09-423-351C-63	Sequence 63, Appl
44	26	48.1	15	3	US-09-423-351C-64	Sequence 64, Appl
45	25	46.3	7	2	US-09-257-069-5	Sequence 5, Appli
46	25	46.3	7	2	US-09-518-737-5	Sequence 5, Appli
47	25	46.3	7	2	US-10-007-790-5	Sequence 5, Appli
48	25	46.3	10	1	US-08-208-886C-87	Sequence 87, Appl
49	25	46.3	10	1	US-08-704-744-89	Sequence 89, Appl
50	25	46.3	10	1	US-08-469-557-68	Sequence 68, Appl
51	25	46.3	10	1	US-08-290-793B-68	Sequence 68, Appl
52	25	46.3	10	2	US-09-602-812A-7	Sequence 7, Appli
53	25	46.3	11	1	US-07-942-245-496	Sequence 496, App
54	25	46.3	11	2	US-09-075-257A-3	Sequence 3, Appli
55	25	46.3	11	2	US-09-075-257A-4	Sequence 4, Appli
56	25	46.3	11	2	US-09-534-639-3	Sequence 3, Appli
57	25	46.3	11	2	US-09-534-639-4	Sequence 4, Appli
58	25	46.3	11	2	US-09-692-170C-3	Sequence 3, Appli
59	25	46.3	11	2	US-09-692-170C-4	Sequence 4, Appli
60	25	46.3	11	2	US-10-405-231A-3	Sequence 3, Appli

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This page gives you Search Results detail for the Application 10661366 and Search Result us-10-661-366 6.closed.rapbm.

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OM protein - protein search, using sw model

Run on: August 9, 2006, 07:35:38 ; Search time 79.5082 Seconds
(without alignments)
58.260 Million cell updates/sec

Title: US-10-661-366-6
Perfect score: 54
Sequence: 1 GYTFTSQDIN 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 395127

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Database : Published_Applications_AA_Main:*
1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	54	100.0	10	5 US-10-661-366-6	Sequence 6, Appli

2	48	88.9	10	5	US-10-726-332-125	Sequence 125, App
3	40	74.1	10	4	US-10-307-276B-31	Sequence 31, Appl
4	40	74.1	10	6	US-11-061-956-31	Sequence 31, Appl
5	40	74.1	10	6	US-11-036-098-8	Sequence 8, Appli
6	38	70.4	10	5	US-10-764-428-14	Sequence 14, Appl
7	36	66.7	10	5	US-10-996-316-152	Sequence 152, App
8	36	66.7	10	6	US-11-171-567-152	Sequence 152, App
9	35	64.8	10	3	US-09-056-160B-1	Sequence 1, Appli
10	35	64.8	10	4	US-10-234-671-1	Sequence 1, Appli
11	35	64.8	10	4	US-10-239-656-14	Sequence 14, Appl
12	35	64.8	10	4	US-10-018-245A-1	Sequence 1, Appli
13	35	64.8	10	4	US-10-723-434-112	Sequence 112, App
14	35	64.8	10	4	US-10-723-434-116	Sequence 116, App
15	35	64.8	10	5	US-10-764-428-15	Sequence 15, Appl
16	35	64.8	10	5	US-10-849-615-23	Sequence 23, Appl
17	35	64.8	10	5	US-10-861-049-43	Sequence 43, Appl
18	35	64.8	10	5	US-10-974-591-1	Sequence 1, Appli
19	35	64.8	10	5	US-10-895-135-20	Sequence 20, Appl
20	35	64.8	10	6	US-11-021-874-43	Sequence 43, Appl
21	35	64.8	10	6	US-11-120-338-10	Sequence 10, Appl
22	35	64.8	10	6	US-11-106-820-10	Sequence 10, Appl
23	35	64.8	10	6	US-11-190-364-10	Sequence 10, Appl
24	35	64.8	10	6	US-11-147-780-10	Sequence 10, Appl
25	35	64.8	10	6	US-11-143-386-10	Sequence 10, Appl
26	35	64.8	13	4	US-10-468-496-1798	Sequence 1798, Ap
27	35	64.8	13	4	US-10-468-496-1799	Sequence 1799, Ap
28	34	63.0	10	4	US-10-723-434-130	Sequence 130, App
29	34	63.0	10	5	US-10-687-035-21	Sequence 21, Appl
30	34	63.0	10	5	US-10-700-632-58	Sequence 58, Appl
31	33	61.1	10	4	US-10-436-782-6	Sequence 6, Appli
32	33	61.1	10	5	US-10-729-441-53	Sequence 53, Appl
33	33	61.1	10	5	US-10-996-316-116	Sequence 116, App
34	33	61.1	10	5	US-10-996-316-146	Sequence 146, App
35	33	61.1	10	5	US-10-897-406-53	Sequence 53, Appl
36	33	61.1	10	5	US-10-932-334-53	Sequence 53, Appl
37	33	61.1	10	6	US-11-004-795A-6	Sequence 6, Appli
38	33	61.1	10	6	US-11-004-794A-6	Sequence 6, Appli
39	33	61.1	10	6	US-11-171-567-116	Sequence 116, App
40	33	61.1	10	6	US-11-171-567-146	Sequence 146, App
41	33	61.1	11	5	US-10-879-994-83	Sequence 83, Appl
42	33	61.1	13	4	US-10-468-496-1797	Sequence 1797, Ap
43	33	61.1	13	4	US-10-468-496-1866	Sequence 1866, Ap
44	33	61.1	13	4	US-10-468-496-1867	Sequence 1867, Ap
45	33	61.1	13	4	US-10-468-496-1868	Sequence 1868, Ap
46	33	61.1	13	4	US-10-468-496-1936	Sequence 1936, Ap
47	33	61.1	13	4	US-10-468-496-1937	Sequence 1937, Ap
48	33	61.1	13	4	US-10-468-496-1938	Sequence 1938, Ap
49	32	59.3	10	3	US-09-900-590-34	Sequence 34, Appl
50	32	59.3	10	4	US-10-160-506-1	Sequence 1, Appli
51	32	59.3	10	4	US-10-305-231-34	Sequence 34, Appl
52	32	59.3	10	4	US-10-463-847-34	Sequence 34, Appl
53	32	59.3	10	4	US-10-624-153-19	Sequence 19, Appl
54	32	59.3	10	4	US-10-449-379-1	Sequence 1, Appli
55	32	59.3	10	4	US-10-688-015-1	Sequence 1, Appli
56	32	59.3	10	4	US-10-327-598-443	Sequence 443, App
57	32	59.3	10	4	US-10-160-505-1	Sequence 1, Appli
58	32	59.3	10	6	US-11-152-846-15	Sequence 15, Appl
59	32	59.3	10	6	US-11-194-989-28	Sequence 28, Appl
60	32	59.3	10	6	US-11-195-207-28	Sequence 28, Appl
61	32	59.3	10	6	US-11-218-813-1	Sequence 1, Appli
62	31	57.4	9	4	US-10-467-253-17	Sequence 17, Appl

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OM protein - protein search, using sw model

Run on: August 9, 2006, 07:36:48 ; Search time 12.623 Seconds
(without alignments)
53.325 Million cell updates/sec

Title: US-10-661-366-6
Perfect score: 54
Sequence: 1 GYTFTSQDIN 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 239914 seqs, 67312017 residues

Total number of hits satisfying chosen parameters: 27373

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Database : Published_Applications_AA_New:*
1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
8: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
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1	36	66.7	10	7	US-11-061-841-235	Sequence 235, App
2	35	64.8	10	7	US-11-254-182-60	Sequence 60, Appl
3	35	64.8	10	7	US-11-106-762-14	Sequence 14, Appl
4	35	64.8	10	7	US-11-291-698A-50	Sequence 50, Appl
5	33	61.1	10	7	US-11-196-917A-4	Sequence 4, Appli
6	33	61.1	10	7	US-11-196-917A-78	Sequence 78, Appl
7	33	61.1	10	7	US-11-196-917A-79	Sequence 79, Appl
8	33	61.1	10	7	US-11-196-917A-87	Sequence 87, Appl
9	33	61.1	10	7	US-11-196-917A-95	Sequence 95, Appl
10	33	61.1	10	7	US-11-196-917A-140	Sequence 140, App
11	33	61.1	10	7	US-11-196-917A-191	Sequence 191, App
12	33	61.1	14	7	US-11-196-917A-166	Sequence 166, App
13	33	61.1	14	7	US-11-196-917A-167	Sequence 167, App
14	32	59.3	10	7	US-11-219-563-1	Sequence 1, Appli
15	29	53.7	10	7	US-11-219-563-93	Sequence 93, Appl
16	29	53.7	10	7	US-11-196-917A-85	Sequence 85, Appl
17	29	53.7	10	7	US-11-196-917A-86	Sequence 86, Appl
18	29	53.7	10	7	US-11-196-917A-91	Sequence 91, Appl
19	29	53.7	10	7	US-11-196-917A-92	Sequence 92, Appl
20	28	51.9	10	7	US-11-061-841-229	Sequence 229, App
21	28	51.9	10	7	US-11-061-841-231	Sequence 231, App
22	28	51.9	10	7	US-11-061-841-233	Sequence 233, App
23	28	51.9	10	7	US-11-061-841-234	Sequence 234, App
24	28	51.9	10	7	US-11-061-841-236	Sequence 236, App
25	28	51.9	10	7	US-11-061-841-241	Sequence 241, App
26	28	51.9	10	7	US-11-061-841-243	Sequence 243, App
27	28	51.9	10	7	US-11-061-841-245	Sequence 245, App
28	28	51.9	10	7	US-11-196-917A-88	Sequence 88, Appl
29	28	51.9	10	7	US-11-196-917A-90	Sequence 90, Appl
30	28	51.9	10	7	US-11-196-917A-93	Sequence 93, Appl
31	27	50.0	10	7	US-11-196-917A-81	Sequence 81, Appl
32	27	50.0	10	7	US-11-196-917A-89	Sequence 89, Appl
33	27	50.0	15	7	US-11-251-340-36	Sequence 36, Appl
34	26	48.1	10	6	US-10-528-172-3	Sequence 3, Appli
35	26	48.1	10	7	US-11-196-917A-84	Sequence 84, Appl
36	26	48.1	10	7	US-11-196-917A-96	Sequence 96, Appl
37	25	46.3	10	6	US-10-981-300-57	Sequence 57, Appl
38	25	46.3	10	6	US-10-544-050-38	Sequence 38, Appl
39	25	46.3	10	6	US-10-542-508-4	Sequence 4, Appli
40	25	46.3	10	7	US-11-254-182-7	Sequence 7, Appli
41	25	46.3	10	7	US-11-335-474-6	Sequence 6, Appli
42	25	46.3	10	7	US-11-295-229-7	Sequence 7, Appli
43	25	46.3	10	7	US-11-196-917A-80	Sequence 80, Appl
44	25	46.3	10	7	US-11-154-091-7	Sequence 7, Appli
45	24	44.4	9	7	US-11-134-871-2480	Sequence 2480, Ap
46	24	44.4	10	6	US-10-542-508-10	Sequence 10, Appl
47	24	44.4	10	7	US-11-219-563-29	Sequence 29, Appl
48	24	44.4	10	7	US-11-219-563-99	Sequence 99, Appl
49	24	44.4	10	7	US-11-196-917A-77	Sequence 77, Appl
50	24	44.4	10	7	US-11-196-917A-82	Sequence 82, Appl
51	24	44.4	10	7	US-11-196-917A-94	Sequence 94, Appl
52	23	42.6	9	6	US-10-991-309B-49	Sequence 49, Appl
53	23	42.6	9	6	US-10-537-642-399	Sequence 399, App
54	23	42.6	9	7	US-11-263-230-6	Sequence 6, Appli
55	23	42.6	9	7	US-11-263-230-16	Sequence 16, Appl
56	23	42.6	9	7	US-11-339-605-38	Sequence 38, Appl
57	23	42.6	9	7	US-11-313-152-195	Sequence 195, App
58	23	42.6	9	7	US-11-396-565-16	Sequence 16, Appl
59	23	42.6	10	6	US-10-981-300-59	Sequence 59, Appl
60	23	42.6	10	6	US-10-991-309B-52	Sequence 52, Appl

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OM protein - protein search, using sw model

Run on: August 9, 2006, 06:51:47 ; Search time 13.7705 Seconds
(without alignments)
69.872 Million cell updates/sec

Title: US-10-661-366-6
Perfect score: 54
Sequence: 1 GYTFTSQDIN 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 2523

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Database : PIR_80:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	25	46.3	10	2	D61440	polygalacturonase
2	25	46.3	11	2	A40795	glycoprotein H-a -
3	24	44.4	12	2	S26548	T-cell receptor be
4	24	44.4	12	2	S47391	T-cell antigen rec
5	24	44.4	12	2	S47394	T-cell antigen rec
6	24	44.4	12	2	S47395	T-cell antigen rec
7	23	42.6	15	2	PH1616	Ig H chain V-D-J r
8	21	38.9	11	2	B49164	chromogranin-B - r

9	20	37.0	9	2	A24244	adipokinetic hormo
10	20	37.0	14	2	A60622	somatostatin - spo
11	20	37.0	14	2	A60840	somatostatin I - E
12	20	37.0	14	2	C60414	somatostatin - sli
13	20	37.0	14	2	B60842	somatostatin I - c
14	20	37.0	14	2	S00172	somatostatin I - s
15	20	37.0	15	2	PA0097	starch phosphoryla
16	19	35.2	9	1	AKLQIM	locustamyoinhibiti
17	19	35.2	9	2	A57444	neuropeptide Grb-A
18	18	33.3	9	2	G85802	hypothetical prote
19	18	33.3	10	2	S62880	polygalacturonase
20	18	33.3	11	2	S14087	parasporal crystal
21	18	33.3	12	2	S26544	T-cell receptor be
22	18	33.3	12	2	S26547	T-cell receptor be
23	18	33.3	12	2	S26546	T-cell receptor be
24	18	33.3	12	2	S26541	T-cell receptor be
25	18	33.3	12	2	PH1458	T-cell receptor be
26	18	33.3	12	2	PH1462	T-cell receptor be
27	18	33.3	12	2	PH1461	T-cell receptor be
28	18	33.3	12	2	PH1457	T-cell receptor be
29	18	33.3	12	2	PH1459	T-cell receptor be
30	18	33.3	12	2	PN0170	alcohol dehydrogen
31	18	33.3	12	2	PN0160	ribosomal protein
32	18	33.3	13	2	C47630	Ig kappa chain J r
33	18	33.3	13	2	A33933	Ig kappa chain J r
34	18	33.3	14	2	S39932	S-allele-associate
35	18	33.3	14	2	S39930	S-allele-associate
36	18	33.3	14	2	B58502	36K kidney stone p
37	18	33.3	14	2	PL0152	metal-binding prot
38	18	33.3	14	2	S29486	GTP-binding protei
39	18	33.3	14	2	S23639	Ig kappa chain J s
40	18	33.3	14	2	PC4376	telomeric and tetr
41	18	33.3	14	2	S39931	S-allele-associate
42	18	33.3	15	2	A56970	GLYMA1 - soybean (
43	18	33.3	15	2	PA0093	enniatin synthetas
44	17	31.5	7	2	A60139	fatty-acid synthas
45	17	31.5	13	2	PU0038	alpha-peptide/alg
46	17	31.5	13	2	PT0263	Ig heavy chain CRD
47	17	31.5	13	2	PT0304	Ig heavy chain CRD
48	17	31.5	15	2	PH1319	Ig heavy chain DJ
49	17	31.5	15	2	S29487	GTP-binding protei
50	17	31.5	15	2	PH1314	Ig heavy chain DJ
51	17	31.5	15	2	A36279	chemoattractant pr
52	16	29.6	8	2	A33995	adipokinetic hormo
53	16	29.6	8	2	B44960	neuropeptide Led-C
54	16	29.6	8	2	S08996	hypertrehalosemic
55	16	29.6	8	2	B49823	adipokinetic hormo
56	16	29.6	8	2	PH0803	T-cell receptor al
57	16	29.6	9	2	PT0231	Ig heavy chain CDR
58	16	29.6	10	2	B33995	hypotrehalosemic h
59	16	29.6	10	2	JC1416	hypertrehalosemic
60	16	29.6	10	2	S09138	hypertrehalosemic
61	16	29.6	10	2	A31571	hypertrehalosemic/
62	16	29.6	10	2	B61440	polygalacturonase
63	16	29.6	10	2	G60589	sperm-activating p
64	16	29.6	11	2	S54347	tubulin beta chain
65	16	29.6	12	2	B44818	extracellular lipa
66	16	29.6	12	2	S01122	photosystem II 3.7
67	16	29.6	12	2	PT0216	T-cell receptor be
68	16	29.6	12	2	E58502	43.2K bile stone p
69	16	29.6	12	2	B58503	outer membrane por

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OM protein - protein search, using sw model

Run on: August 9, 2006, 06:40:52 ; Search time 111.475 Seconds
(without alignments)
82.979 Million cell updates/sec

Title: US-10-661-366-6
Perfect score: 54
Sequence: 1·GYTFTSQDIN 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 8966

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Database : UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	29	53.7	13	1	SAL2A_ONCMY P82238 oncorhynchu
2	29	53.7	13	1	SAL2B_ONCMY P82239 oncorhynchu
3	25	46.3	10	2	Q7M501_9EURO Q7m501 aspergillus
4	23	42.6	11	1	CAP5_CANAL P83782 candida alb

5	22	40.7	9	2	P83529_LACSN	P83529	lactobacill
6	22	40.7	10	2	Q8VIL8_MOUSE	Q8vil8	mus musculu
7	22	40.7	12	1	XYLA_STRVN	P14405	streptomyce
8	21	38.9	10	1	SC46_TITCA	P84686	tityus camb
9	21	38.9	11	2	Q9QVH3_9MURI	Q9qvh3	rattus sp.
10	21	38.9	12	2	Q7RQJ4_PLAYO	Q7rqj4	plasmodium
11	21	38.9	15	2	Q8AXQ9_XENLA	Q8axq9	xenopus lae
12	20	37.0	9	1	AKH_HELZE	P67787	heliiothis z
13	20	37.0	14	1	CWP27_TOBAC	P82435	nicotiana t
14	20	37.0	14	1	SMS1_ANGAN	P69134	anguilla an
15	20	37.0	14	1	SMS1_MYOSC	P69132	myoxocephal
16	20	37.0	14	1	SMS1_ONCKI	P69133	oncorhynchu
17	20	37.0	14	1	SMS_ALLMI	P61298	alligator m
18	20	37.0	14	1	SMS_TRASC	P61299	trachemys s
19	20	37.0	14	2	Q76W18_9FLAV	Q76w18	gb virus c.
20	20	37.0	14	2	Q76W19_9FLAV	Q76w19	gb virus c.
21	20	37.0	14	2	Q76W20_9FLAV	Q76w20	gb virus c.
22	20	37.0	14	2	Q76W21_9FLAV	Q76w21	gb virus c.
23	20	37.0	14	2	Q76W22_9FLAV	Q76w22	gb virus c.
24	20	37.0	14	2	Q76W23_9FLAV	Q76w23	gb virus c.
25	20	37.0	14	2	Q76W24_9FLAV	Q76w24	gb virus c.
26	20	37.0	14	2	Q76W25_9FLAV	Q76w25	gb virus c.
27	20	37.0	14	2	Q76W28_9FLAV	Q76w28	gb virus c.
28	20	37.0	14	2	Q76W29_9FLAV	Q76w29	gb virus c.
29	20	37.0	14	2	Q76W30_9FLAV	Q76w30	gb virus c.
30	20	37.0	14	2	Q76W34_9FLAV	Q76w34	gb virus c.
31	20	37.0	14	2	Q76W36_9FLAV	Q76w36	gb virus c.
32	20	37.0	14	2	Q76W38_9FLAV	Q76w38	gb virus c.
33	20	37.0	14	2	Q76W44_9FLAV	Q76w44	gb virus c.
34	20	37.0	14	2	Q9W982_9FLAV	Q9w982	gb virus c.
35	20	37.0	14	2	Q7LZD4_HYDCO	Q7lzd4	hydrolagus
36	20	37.0	15	2	Q4XG09_PLACH	Q4xg09	plasmodium
37	20	37.0	15	2	Q7RHB9_PLAYO	Q7rhb9	plasmodium
38	19	35.2	8	2	Q9S6D5_ECOLI	Q9s6d5	escherichia
39	19	35.2	9	1	LMIP_LOCFI	P31799	locusta mig
40	19	35.2	9	2	Q7M3N9_GRYBI	Q7m3n9	gryllus bim
41	19	35.2	11	2	Q5DQJ8_9LILI	Q5dqj8	nenga gajah
42	19	35.2	12	1	CWP29_TOBAC	P82437	nicotiana t
43	19	35.2	12	2	Q5DQJ9_9LILI	Q5dqj9	nenga gajah
44	19	35.2	14	2	Q7RB25_PLAYO	Q7rb25	plasmodium
45	19	35.2	15	2	Q7S007_NEUCR	Q7s007	neurospora
46	19	35.2	15	2	Q9QV00_9MURI	Q9qv00	rattus sp.
47	18.5	34.3	13	2	Q70Y65_9LAMI	Q70y65	tectona gra
48	18	33.3	8	1	ALL5_CYDPO	P82156	cydia pomon
49	18	33.3	8	2	Q7Z7I9_HUMAN	Q7z7i9	homo sapien
50	18	33.3	9	1	CWP06_PHAVU	P80765	phaseolus v
51	18	33.3	9	2	Q8X4G1_ECO57	Q8x4g1	escherichia
52	18	33.3	10	1	ESTA_SCHGA	P81012	schizaphis
53	18	33.3	10	2	Q7M500_9EURO	Q7m500	aspergillus
54	18	33.3	10	2	Q6EX62_HYPSU	Q6ex62	hyptis suav
55	18	33.3	11	1	CWP22_ARATH	P80843	arabidopsis
56	18	33.3	11	2	Q6YHP4_9MARC	Q6yhp4	chiloscyphu
57	18	33.3	11	2	Q70Y64_9LAMI	Q70y64	plectranthu
58	18	33.3	12	2	Q7M4Y0_FUSSP	Q7m4y0	fusarium sp
59	18	33.3	12	2	Q7M4Z9_FUSSP	Q7m4z9	fusarium sp
60	18	33.3	12	2	Q70Y58_9LAMI	Q70y58	clinopodium
61	18	33.3	12	2	Q53VP7_MOUSE	Q53vp7	mus musculu
62	18	33.3	12	2	Q6WR52_ASIOT	Q6wr52	asio otus (
63	18	33.3	13	1	UN12_CLOPA	P81353	clostridium
64	18	33.3	13	2	Q8I2E2_PLAF7	Q8i2e2	plasmodium
65	18	33.3	14	2	Q7M261_PYRPY	Q7m261	pyrus pyrif

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OM protein - protein search, using sw model

Run on: August 9, 2006, 07:45:18 ; Search time 25.256 Seconds
(without alignments)
181.033 Million cell updates/sec

Title: US-10-661-366-6
Perfect score: 54
Sequence: 1 GYTFTSQDIN 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : A_Geneseq_8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	54	100.0	10	9	ADY75171	Ady75171 Antibody
2	54	100.0	125	9	ADY75166	Ady75166 Antibody
3	48	88.9	10	8	ADP47210	Adp47210 Human pho
4	48	88.9	92	4	AAM20077	Aam20077 Peptide #
5	48	88.9	92	4	AAM33913	Aam33913 Peptide #
6	48	88.9	92	4	ABG55467	Abg55467 Human liv
7	48	88.9	92	5	ABG43604	Abg43604 Human pep
8	48	88.9	98	3	AAy50958	Aay50958 Human FVI
9	48	88.9	98	5	ABG78170	Abg78170 Human Fv
10	48	88.9	98	5	ABG91861	Abg91861 Human ant
11	48	88.9	98	6	ABO27070	Abo27070 Human ger
12	48	88.9	98	7	ADF10108	Adf10108 Antibody
13	48	88.9	98	7	ADF09898	Adf09898 Antibody
14	48	88.9	98	7	ADF10006	Adf10006 VEGF anti
15	48	88.9	98	7	ADK18866	Adk18866 Anti-huma
16	48	88.9	98	7	ADK18920	Adk18920 Anti-huma
17	48	88.9	98	7	ADK18924	Adk18924 Anti-huma
18	48	88.9	98	7	ADK18918	Adk18918 Anti-huma
19	48	88.9	98	7	ADK18937	Adk18937 Anti-huma
20	48	88.9	98	7	ADK18949	Adk18949 Anti-huma
21	48	88.9	98	7	ADK18938	Adk18938 Anti-huma
22	48	88.9	98	7	ADK18872	Adk18872 Anti-huma
23	48	88.9	98	7	ADK18865	Adk18865 Anti-huma
24	48	88.9	98	7	ADK18871	Adk18871 Anti-huma
25	48	88.9	98	7	ADK18950	Adk18950 Anti-huma
26	48	88.9	98	7	ADK18926	Adk18926 Anti-huma
27	48	88.9	98	7	ADJ80283	Adj80283 VH gene 1
28	48	88.9	98	9	ADY75288	Ady75288 Protein e
29	48	88.9	98	10	AEE47526	Aee47526 Human CDR
30	48	88.9	98	10	AEF18663	Aef18663 HAHA prot
31	48	88.9	99	7	ADK18577	Adk18577 Anti-huma
32	48	88.9	99	9	AED06853	Aed06853 Human ant
33	48	88.9	99	10	AEF18417	Aef18417 HAHA prot
34	48	88.9	116	2	AAR79241	Aar79241 Heavy cha
35	48	88.9	117	2	AAR66302	Aar66302 Human imm
36	48	88.9	119	6	ABJ18572	Abj18572 Gangliosi
37	48	88.9	119	6	ABJ18570	Abj18570 Gangliosi
38	48	88.9	119	10	AEF12980	Aef12980 Mouse E34
39	48	88.9	120	4	AAB62747	Aab62747 Human HIV
40	48	88.9	122	6	ABR55829	Abr55829 Heavy cha
41	48	88.9	123	9	AED87298	Aed87298 Fv2A7 hea
42	48	88.9	125	7	ADK18776	Adk18776 Anti-huma
43	48	88.9	125	7	ADK18814	Adk18814 Anti-huma
44	48	88.9	125	7	ADK18948	Adk18948 Anti-huma
45	48	88.9	125	7	ADK18614	Adk18614 Anti-huma
46	48	88.9	125	7	ADK18779	Adk18779 Anti-huma
47	48	88.9	125	7	ADK18919	Adk18919 Anti-huma
48	48	88.9	125	7	ADK18816	Adk18816 Anti-huma
49	48	88.9	125	7	ADK18624	Adk18624 Anti-huma
50	48	88.9	125	7	ADK18813	Adk18813 Anti-huma
51	48	88.9	125	8	ADL25444	Adl25444 Human mAb
52	48	88.9	125	8	ADL25392	Adl25392 Human mAb
53	48	88.9	126	7	ADK18864	Adk18864 Anti-huma
54	48	88.9	126	7	ADK18597	Adk18597 Anti-huma
55	48	88.9	126	7	ADK18870	Adk18870 Anti-huma
56	48	88.9	126	7	ADK18595	Adk18595 Anti-huma
57	48	88.9	126	7	ADK18812	Adk18812 Anti-huma

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OM protein - protein search, using sw model

Run on: August 9, 2006, 08:17:00 ; Search time 6.58703 Seconds
(without alignments)
132.883 Million cell updates/sec

Title: US-10-661-366-6
Perfect score: 54
Sequence: 1 GYTFTSQDIN 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Issued_Patents_AA:*
1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	48	88.9	96	2 US-10-194-975-3	Sequence 3, Appli

2	48	88.9	116	1	US-08-888-366-2	Sequence 2, Appli
3	48	88.9	117	2	US-08-545-809A-96	Sequence 96, Appl
4	48	88.9	117	2	US-09-515-697-96	Sequence 96, Appl
5	43	79.6	127	2	US-09-513-999C-4122	Sequence 4122, Ap
6	43	79.6	134	2	US-09-471-276-849	Sequence 849, App
7	42	77.8	112	1	US-07-942-245-23	Sequence 23, Appl
8	42	77.8	121	2	US-09-232-290-59	Sequence 59, Appl
9	41	75.9	200	7	5189147-8	Patent No. 5189147
10	41	75.9	561	2	US-09-192-545-2	Sequence 2, Appli
11	40	74.1	115	1	US-07-942-245-22	Sequence 22, Appl
12	40	74.1	124	2	US-09-232-290-51	Sequence 51, Appl
13	39	72.2	118	1	US-08-300-386A-64	Sequence 64, Appl
14	39	72.2	118	2	US-08-931-645-64	Sequence 64, Appl
15	39	72.2	118	5	PCT-US95-11235-64	Sequence 64, Appl
16	39	72.2	119	1	US-08-478-039-65	Sequence 65, Appl
17	39	72.2	119	1	US-08-476-349A-65	Sequence 65, Appl
18	38	70.4	118	2	US-08-908-469-110	Sequence 110, App
19	38	70.4	118	2	US-08-908-469-114	Sequence 114, App
20	38	70.4	119	2	US-09-328-352-5881	Sequence 5881, Ap
21	38	70.4	487	2	US-09-248-796A-16516	Sequence 16516, A
22	38	70.4	510	2	US-09-710-279-2860	Sequence 2860, Ap
23	37	68.5	20	2	US-09-556-605-6	Sequence 6, Appli
24	37	68.5	98	2	US-10-194-975-47	Sequence 47, Appl
25	37	68.5	113	2	US-09-434-870-4	Sequence 4, Appli
26	37	68.5	119	2	US-09-556-605-1	Sequence 1, Appli
27	37	68.5	120	1	US-08-602-725-27	Sequence 27, Appl
28	37	68.5	128	1	US-08-478-039-73	Sequence 73, Appl
29	37	68.5	128	1	US-08-478-039-102	Sequence 102, App
30	37	68.5	128	1	US-08-476-349A-73	Sequence 73, Appl
31	37	68.5	128	1	US-08-476-349A-102	Sequence 102, App
32	36	66.7	98	2	US-08-881-037-64	Sequence 64, Appl
33	36	66.7	98	2	US-10-194-975-4	Sequence 4, Appli
34	36	66.7	98	2	US-10-330-613A-53	Sequence 53, Appl
35	36	66.7	113	2	US-08-881-037-18	Sequence 18, Appl
36	36	66.7	117	2	US-08-545-809A-105	Sequence 105, App
37	36	66.7	117	2	US-09-515-697-105	Sequence 105, App
38	36	66.7	118	2	US-09-726-219A-165	Sequence 165, App
39	36	66.7	118	2	US-09-196-522-165	Sequence 165, App
40	36	66.7	120	2	US-09-513-999C-4111	Sequence 4111, Ap
41	36	66.7	121	2	US-08-881-037-65	Sequence 65, Appl
42	36	66.7	121	2	US-09-513-999C-4115	Sequence 4115, Ap
43	36	66.7	391	2	US-09-248-796A-15903	Sequence 15903, A
44	36	66.7	1833	2	US-08-479-722B-2	Sequence 2, Appli
45	36	66.7	1833	2	US-09-592-685-2	Sequence 2, Appli
46	36	66.7	1833	5	PCT-US95-02251-18	Sequence 18, Appl
47	35	64.8	10	2	US-08-908-469-1	Sequence 1, Appli
48	35	64.8	92	2	US-08-783-853A-84	Sequence 84, Appl
49	35	64.8	92	2	US-09-344-050-84	Sequence 84, Appl
50	35	64.8	98	2	US-09-534-717-612	Sequence 612, App
51	35	64.8	98	2	US-09-534-717-613	Sequence 613, App
52	35	64.8	98	2	US-09-534-717-614	Sequence 614, App
53	35	64.8	108	2	US-09-899-896-1	Sequence 1, Appli
54	35	64.8	108	2	US-09-899-896-3	Sequence 3, Appli
55	35	64.8	112	2	US-08-783-853A-20	Sequence 20, Appl
56	35	64.8	112	2	US-08-545-809A-113	Sequence 113, App
57	35	64.8	112	2	US-09-344-050-20	Sequence 20, Appl
58	35	64.8	112	2	US-09-515-697-113	Sequence 113, App
59	35	64.8	114	1	US-08-652-558-52	Sequence 52, Appl
60	35	64.8	116	2	US-10-138-727A-2	Sequence 2, Appli
61	35	64.8	116	2	US-10-138-727A-4	Sequence 4, Appli
62	35	64.8	116	2	US-10-138-727A-6	Sequence 6, Appli

SCORE Search Results Details for Application 10661366 and Search Result us-10-661-366-6.ra

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This page gives you Search Results detail for the Application 10661366 and Search Result us-10-661-366-6.ra

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OM protein - protein search, using sw model

Run on: August 9, 2006, 09:01:05 ; Search time 21.3993 Seconds
(without alignments)
216.462 Million cell updates/sec

Title: US-10-661-366-6
Perfect score: 54
Sequence: 1 GYTFTSQDIN 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Published_Applications_AA_Main:*
1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	54	100.0	10	5	US-10-661-366-6	Sequence 6, Appli
2	54	100.0	125	5	US-10-661-366-1	Sequence 1, Appli
3	48	88.9	10	5	US-10-726-332-125	Sequence 125, App

4	48	88.9	92	3	US-09-864-761-47202	Sequence 47202, A
5	48	88.9	96	4	US-10-194-975-3	Sequence 3, Appli
6	48	88.9	98	4	US-10-041-860-289	Sequence 289, App
7	48	88.9	98	4	US-10-041-860-290	Sequence 290, App
8	48	88.9	98	4	US-10-041-860-295	Sequence 295, App
9	48	88.9	98	4	US-10-041-860-296	Sequence 296, App
10	48	88.9	98	4	US-10-041-860-342	Sequence 342, App
11	48	88.9	98	4	US-10-041-860-344	Sequence 344, App
12	48	88.9	98	4	US-10-041-860-348	Sequence 348, App
13	48	88.9	98	4	US-10-041-860-350	Sequence 350, App
14	48	88.9	98	4	US-10-041-860-361	Sequence 361, App
15	48	88.9	98	4	US-10-041-860-362	Sequence 362, App
16	48	88.9	98	4	US-10-041-860-373	Sequence 373, App
17	48	88.9	98	4	US-10-041-860-374	Sequence 374, App
18	48	88.9	98	4	US-10-308-817-43	Sequence 43, Appl
19	48	88.9	98	4	US-10-032-037B-45	Sequence 45, Appl
20	48	88.9	98	4	US-10-029-988B-45	Sequence 45, Appl
21	48	88.9	98	4	US-10-032-423A-45	Sequence 45, Appl
22	48	88.9	98	4	US-10-453-698-43	Sequence 43, Appl
23	48	88.9	98	4	US-10-029-926B-45	Sequence 45, Appl
24	48	88.9	98	4	US-10-379-392-3	Sequence 3, Appli
25	48	88.9	98	6	US-11-054-669-3	Sequence 3, Appli
26	48	88.9	98	6	US-11-004-590-3	Sequence 3, Appli
27	48	88.9	99	4	US-10-041-860-1	Sequence 1, Appli
28	48	88.9	99	6	US-11-084-554-23	Sequence 23, Appl
29	48	88.9	99	6	US-11-136-250-23	Sequence 23, Appl
30	48	88.9	119	5	US-10-473-977-67	Sequence 67, Appl
31	48	88.9	119	6	US-11-226-886-46	Sequence 46, Appl
32	48	88.9	119	6	US-11-159-046-12	Sequence 12, Appl
33	48	88.9	122	4	US-10-269-805-61	Sequence 61, Appl
34	48	88.9	122	5	US-10-982-440-61	Sequence 61, Appl
35	48	88.9	125	4	US-10-041-860-38	Sequence 38, Appl
36	48	88.9	125	4	US-10-041-860-48	Sequence 48, Appl
37	48	88.9	125	4	US-10-041-860-200	Sequence 200, App
38	48	88.9	125	4	US-10-041-860-203	Sequence 203, App
39	48	88.9	125	4	US-10-041-860-237	Sequence 237, App
40	48	88.9	125	4	US-10-041-860-238	Sequence 238, App
41	48	88.9	125	4	US-10-041-860-240	Sequence 240, App
42	48	88.9	125	4	US-10-041-860-343	Sequence 343, App
43	48	88.9	125	4	US-10-041-860-372	Sequence 372, App
44	48	88.9	125	4	US-10-665-383-2	Sequence 2, Appli
45	48	88.9	125	4	US-10-665-383-54	Sequence 54, Appl
46	48	88.9	126	4	US-10-041-860-19	Sequence 19, Appl
47	48	88.9	126	4	US-10-041-860-21	Sequence 21, Appl
48	48	88.9	126	4	US-10-041-860-199	Sequence 199, App
49	48	88.9	126	4	US-10-041-860-201	Sequence 201, App
50	48	88.9	126	4	US-10-041-860-236	Sequence 236, App
51	48	88.9	126	4	US-10-041-860-288	Sequence 288, App
52	48	88.9	126	4	US-10-041-860-294	Sequence 294, App
53	48	88.9	126	4	US-10-665-383-18	Sequence 18, Appl
54	48	88.9	126	4	US-10-665-383-22	Sequence 22, Appl
55	48	88.9	127	4	US-10-041-860-44	Sequence 44, Appl
56	48	88.9	127	4	US-10-041-860-205	Sequence 205, App
57	48	88.9	127	4	US-10-041-860-242	Sequence 242, App
58	48	88.9	127	4	US-10-041-860-360	Sequence 360, App
59	48	88.9	127	4	US-10-665-383-66	Sequence 66, Appl
60	48	88.9	138	2	US-08-779-784-31	Sequence 31, Appl
61	48	88.9	138	4	US-10-010-729-67	Sequence 67, Appl
62	48	88.9	139	4	US-10-006-773-13	Sequence 13, Appl
63	48	88.9	146	3	US-09-925-299-1050	Sequence 1050, Ap
64	48	88.9	146	3	US-09-925-299-1050	Sequence 1050, Ap

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OM protein - protein search, using sw model

Run on: August 9, 2006, 09:02:15 ; Search time 3.27645 Seconds
(without alignments)
205.442 Million cell updates/sec

Title: US-10-661-366-6
Perfect score: 54
Sequence: 1 GYTFTSQDIN 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 239914 seqs, 67312017 residues

Total number of hits satisfying chosen parameters: 239914

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Published_Applications_AA_New:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	% Query
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No.	Score	Match	Length	DB	ID	Description
1	48	88.9	81	1	US-09-784-950-82	Sequence 82, Appl
2	48	88.9	92	1	US-09-784-950-83	Sequence 83, Appl
3	48	88.9	96	1	US-09-784-950-84	Sequence 84, Appl
4	48	88.9	98	7	US-11-221-902-54	Sequence 54, Appl
5	48	88.9	138	7	US-11-224-664-31	Sequence 31, Appl
6	48	88.9	199	1	US-09-784-950-29	Sequence 29, Appl
7	48	88.9	203	1	US-09-784-950-27	Sequence 27, Appl
8	41	75.9	269	6	US-10-539-402-1	Sequence 1, Appli
9	39	72.2	245	7	US-11-290-687-47	Sequence 47, Appl
10	36	66.7	10	7	US-11-061-841-235	Sequence 235, App
11	36	66.7	98	7	US-11-221-902-55	Sequence 55, Appl
12	36	66.7	118	7	US-11-375-221-111	Sequence 111, App
13	36	66.7	120	7	US-11-337-300-33	Sequence 33, Appl
14	36	66.7	247	7	US-11-337-300-65	Sequence 65, Appl
15	36	66.7	464	7	US-11-375-221-22	Sequence 22, Appl
16	36	66.7	1052	6	US-10-497-088-21	Sequence 21, Appl
17	36	66.7	1342	6	US-10-497-088-14	Sequence 14, Appl
18	35	64.8	10	7	US-11-254-182-60	Sequence 60, Appl
19	35	64.8	10	7	US-11-106-762-14	Sequence 14, Appl
20	35	64.8	10	7	US-11-291-698A-50	Sequence 50, Appl
21	35	64.8	40	7	US-11-238-281-10	Sequence 10, Appl
22	35	64.8	40	7	US-11-238-281-11	Sequence 11, Appl
23	35	64.8	114	7	US-11-249-296-42	Sequence 42, Appl
24	35	64.8	114	7	US-11-249-296-44	Sequence 44, Appl
25	35	64.8	116	7	US-11-024-877-8	Sequence 8, Appli
26	35	64.8	116	7	US-11-024-877-9	Sequence 9, Appli
27	35	64.8	116	7	US-11-024-877-10	Sequence 10, Appl
28	35	64.8	120	7	US-11-290-687-70	Sequence 70, Appl
29	35	64.8	121	7	US-11-337-300-323	Sequence 323, App
30	35	64.8	121	7	US-11-256-060-2	Sequence 2, Appli
31	35	64.8	122	7	US-11-254-182-28	Sequence 28, Appl
32	35	64.8	122	7	US-11-254-182-29	Sequence 29, Appl
33	35	64.8	122	7	US-11-254-182-74	Sequence 74, Appl
34	35	64.8	122	7	US-11-106-762-2	Sequence 2, Appli
35	35	64.8	122	7	US-11-106-762-11	Sequence 11, Appl
36	35	64.8	122	7	US-11-106-762-12	Sequence 12, Appl
37	35	64.8	122	7	US-11-238-281-7	Sequence 7, Appli
38	35	64.8	122	7	US-11-238-281-8	Sequence 8, Appli
39	35	64.8	122	7	US-11-238-281-40	Sequence 40, Appl
40	35	64.8	122	7	US-11-256-060-4	Sequence 4, Appli
41	35	64.8	122	7	US-11-291-698A-47	Sequence 47, Appl
42	35	64.8	122	7	US-11-291-698A-48	Sequence 48, Appl
43	35	64.8	123	7	US-11-254-182-32	Sequence 32, Appl
44	35	64.8	123	7	US-11-254-182-34	Sequence 34, Appl
45	35	64.8	123	7	US-11-238-281-33	Sequence 33, Appl
46	35	64.8	126	6	US-10-523-295-13	Sequence 13, Appl
47	35	64.8	126	6	US-10-523-295-14	Sequence 14, Appl
48	35	64.8	126	6	US-10-523-295-15	Sequence 15, Appl
49	35	64.8	129	7	US-11-006-808-45	Sequence 45, Appl
50	35	64.8	130	7	US-11-315-067-34	Sequence 34, Appl
51	35	64.8	130	7	US-11-315-067-35	Sequence 35, Appl
52	35	64.8	136	7	US-11-315-067-2	Sequence 2, Appli
53	35	64.8	136	7	US-11-315-067-8	Sequence 8, Appli
54	35	64.8	140	7	US-11-183-218-62	Sequence 62, Appl
55	35	64.8	250	6	US-10-684-237-2	Sequence 2, Appli
56	35	64.8	251	7	US-11-337-300-222	Sequence 222, App
57	35	64.8	253	7	US-11-024-877-2	Sequence 2, Appli
58	35	64.8	253	7	US-11-024-877-3	Sequence 3, Appli
59	35	64.8	451	6	US-10-822-231-4	Sequence 4, Appli

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OM protein - protein search, using sw model

Run on: August 9, 2006, 08:00:49 ; Search time 3.92491 Seconds
(without alignments)
245.144 Million cell updates/sec

Title: US-10-661-366-6
Perfect score: 54
Sequence: 1 GYTFTSQDIN 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : PIR_80:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	48	88.9	98	2 S26918	Ig heavy chain V r
2	48	88.9	110	2 PH1670	Ig heavy chain V r
3	48	88.9	117	1 HVMSA1	Ig heavy chain pre
4	48	88.9	127	2 S34014	Ig heavy chain V r
5	48	88.9	136	2 S31600	Ig heavy chain V r
6	45	83.3	111	2 PH0988	Ig heavy chain V r
7	43	79.6	132	2 S31596	Ig heavy chain V r
8	42	77.8	90	2 PH1485	Ig heavy chain V r

9	42	77.8	121	2	A30551	Ig heavy chain V r
10	42	77.8	140	2	PH1486	Ig heavy chain V r
11	42	77.8	140	2	PH1498	Ig heavy chain V r
12	42	77.8	140	2	PH1499	Ig heavy chain V r
13	41	75.9	76	2	B28572	Ig heavy chain V r
14	41	75.9	98	2	B24754	Ig heavy chain V r
15	41	75.9	98	2	A28572	Ig heavy chain V r
16	41	75.9	102	2	PH1491	Ig heavy chain V r
17	41	75.9	102	2	PH1490	Ig heavy chain V r
18	41	75.9	102	2	S42176	Ig gamma chain V r
19	41	75.9	114	2	PH1523	Ig heavy chain V r
20	41	75.9	114	2	PH1522	Ig heavy chain V r
21	41	75.9	118	2	S38565	Ig heavy chain V r
22	41	75.9	118	2	A24754	Ig heavy chain V r
23	41	75.9	119	2	PH1510	Ig heavy chain V r
24	41	75.9	119	2	PH1505	Ig heavy chain V r
25	41	75.9	119	2	PH1518	Ig heavy chain V r
26	41	75.9	119	2	PH1517	Ig heavy chain V r
27	41	75.9	119	2	PH1502	Ig heavy chain V r
28	41	75.9	119	2	PH1500	Ig heavy chain V r
29	41	75.9	119	2	PH1503	Ig heavy chain V r
30	41	75.9	119	2	PH1504	Ig heavy chain V r
31	41	75.9	119	2	PH1520	Ig heavy chain V r
32	41	75.9	120	2	S26789	Ig heavy chain V r
33	41	75.9	121	2	A21854	Ig heavy chain V r
34	41	75.9	121	2	A26405	Ig heavy chain V r
35	41	75.9	135	2	PH1494	Ig heavy chain V r
36	41	75.9	135	2	PH1492	Ig heavy chain V r
37	41	75.9	140	1	HVMSG7	Ig heavy chain pre
38	41	75.9	140	2	PH1483	Ig heavy chain V r
39	41	75.9	140	2	PH1482	Ig heavy chain V r
40	40	74.1	110	2	A32189	Ig heavy chain V r
41	40	74.1	123	2	G48677	Ig heavy chain V-D
42	40	74.1	123	2	F48677	Ig heavy chain V-D
43	40	74.1	123	2	E48677	Ig heavy chain V-D
44	40	74.1	150	2	I47200	Ig heavy chain var
45	39	72.2	125	2	S68170	Ig heavy chain V r
46	39	72.2	140	2	PH1484	Ig heavy chain V r
47	38	70.4	96	2	S17614	Ig heavy chain V r
48	38	70.4	101	2	PH0983	Ig heavy chain V r
49	38	70.4	101	2	PH0982	Ig heavy chain V r
50	38	70.4	104	2	PH0981	Ig heavy chain V r
51	38	70.4	107	2	PH0984	Ig heavy chain V r
52	38	70.4	111	2	S26463	Ig heavy chain V r
53	38	70.4	119	2	PH1521	Ig heavy chain V r
54	38	70.4	119	2	PH1519	Ig heavy chain V r
55	38	70.4	120	2	S09956	Ig heavy chain V-D
56	38	70.4	135	2	A30577	Ig heavy chain pre
57	38	70.4	135	2	PH1493	Ig heavy chain V r
58	38	70.4	138	2	E32513	Ig heavy chain pre
59	38	70.4	140	2	A36194	Ig heavy chain V r
60	38	70.4	140	2	PH1489	Ig heavy chain V r
61	38	70.4	2783	2	T34416	hypothetical prote
62	37	68.5	98	2	H34964	Ig heavy chain V-I
63	37	68.5	98	2	A49051	Ig heavy chain V7
64	37	68.5	116	2	S31667	Ig heavy chain V r
65	37	68.5	117	2	S18554	Ig heavy chain V r
66	37	68.5	119	2	H45722	anti-glycoprotein
67	37	68.5	131	2	S26792	Ig heavy chain V r
68	37	68.5	142	2	S19245	Ig heavy chain pre
69	37	68.5	217	1	VCVXPS	coat protein - pea

SCORE Search Results Details for Application 10661366 and Search Result us-10-661-366-6.rup.

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This page gives you Search Results detail for the Application 10661366 and Search Result us-10-661-366-6.rup.

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OM protein - protein search, using sw model

Run on: August 9, 2006, 07:46:18 ; Search time 30.2389 Seconds
(without alignments)
305.902 Million cell updates/sec

Title: US-10-661-366-6
Perfect score: 54
Sequence: 1 GYTFTSQDIN 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	48	88.9	117	1 HV52_MOUSE	P06327 mus musculu
2	43	79.6	404	2 Q6R7D6_9HERP	Q6r7d6 ostreid her
3	43	79.6	591	2 Q4QQW0_RAT	Q4qqw0 rattus norv
4	42	77.8	458	2 Q5BK05_RAT	Q5bk05 rattus norv

5	41	75.9	120	1	HV03_MOUSE	P01747	mus musculu
6	41	75.9	140	1	HV02_MOUSE	P01746	mus musculu
7	41	75.9	480	2	Q8K0Z4_MOUSE	Q8k0z4	mus musculu
8	40	74.1	415	2	Q2N141_9METZ	Q2n141	suberites f
9	40	74.1	458	2	Q5BJZ2_RAT	Q5bjz2	rattus norv
10	40	74.1	606	2	Q464T5_THEAN	Q464t5	theileria a
11	40	74.1	1013	2	Q9NHZ7_HELPN	Q9nhz7	helicoverpa
12	40	74.1	3463	2	Q7R1E2_GIALA	Q7r1e2	giardia lam
13	39	72.2	99	2	Q2RTU9_RHORU	Q2rtu9	rhodospiril
14	39	72.2	448	2	Q8A5I6_BACTN	Q8a5i6	bacteroides
15	39	72.2	468	2	Q569W9_MOUSE	Q569w9	mus musculu
16	39	72.2	483	2	Q8TOR6_DROME	Q8t0r6	drosophila
17	39	72.2	497	2	Q8WY24_HUMAN	Q8wy24	homo sapien
18	39	72.2	751	2	Q483Y4_COLP3	Q483y4	colwellia p
19	39	72.2	777	2	Q9VXA5_DROME	Q9vxa5	drosophila
20	39	72.2	822	2	Q7KUX2_DROME	Q7kux2	drosophila
21	38	70.4	125	2	Q4Y5Z0_PLACH	Q4y5z0	plasmodium
22	38	70.4	410	2	Q8POR2_STRP8	Q8p0r2	streptococc
23	38	70.4	484	2	Q3SYJ4_MOUSE	Q3syj4	mus musculu
24	38	70.4	486	2	Q9PYN5_GVXN	Q9pyn5	xestia c-ni
25	38	70.4	560	1	Y889_VIBF1	Q5e6g2	vibrio fisc
26	38	70.4	1083	2	Q7RZT2_NEUCR	Q7rzt2	neurospora
27	38	70.4	1390	2	Q8PX84_METMA	Q8px84	methanosarc
28	38	70.4	2693	2	Q8ISF3_CAEEL	Q8isf3	caenorhabdi
29	38	70.4	2708	2	Q8ISF4_CAEEL	Q8isf4	caenorhabdi
30	38	70.4	2713	2	Q86IL0_DICDI	Q86il0	dictyosteli
31	38	70.4	2785	2	Q558U0_DICDI	Q558u0	dictyosteli
32	38	70.4	2798	2	Q4UIN4_THEAN	Q4uin4	theileria a
33	38	70.4	18519	2	Q8ISF6_CAEEL	Q8isf6	caenorhabdi
34	38	70.4	18534	2	Q8ISF7_CAEEL	Q8isf7	caenorhabdi
35	37	68.5	92	2	Q31KM3_SYNPF	Q31km3	synechococc
36	37	68.5	111	2	Q2V0Z6_TAV	Q2v0z6	tomato aspe
37	37	68.5	138	2	Q2WNA1_CLOBE	Q2wna1	clostridium
38	37	68.5	143	2	Q4HSC9_CAMUP	Q4hsc9	campylobact
39	37	68.5	147	2	Q925S3_MOUSE	Q925s3	mus musculu
40	37	68.5	184	2	Q8I609_PLAF7	Q8i609	plasmodium
41	37	68.5	214	2	Q9YPB4_9BROM	Q9ypb4	peanut stun
42	37	68.5	217	1	COAT_PSVJ	P221l6	peanut stun
43	37	68.5	217	2	Q5U8Z1_9BROM	Q5u8z1	peanut stun
44	37	68.5	217	2	Q86801_TAV	Q86801	tomato aspe
45	37	68.5	217	2	Q9YPQ9_9BROM	Q9ypq9	peanut stun
46	37	68.5	217	2	Q9YPR0_9BROM	Q9ypr0	peanut stun
47	37	68.5	218	2	Q4A1H4_TAV	Q4alh4	tomato aspe
48	37	68.5	218	2	Q4A1H5_TAV	Q4alh5	tomato aspe
49	37	68.5	218	2	Q4A1H6_TAV	Q4alh6	tomato aspe
50	37	68.5	218	2	Q4A1H7_TAV	Q4alh7	tomato aspe
51	37	68.5	218	2	Q4A1K2_TAV	Q4alk2	tomato aspe
52	37	68.5	218	2	Q4A1K3_TAV	Q4alk3	tomato aspe
53	37	68.5	218	2	Q4GX43_TAV	Q4gx43	tomato aspe
54	37	68.5	218	2	Q4GX44_TAV	Q4gx44	tomato aspe
55	37	68.5	218	2	Q50HP5_TAV	Q50hp5	tomato aspe
56	37	68.5	218	2	Q50HX9_TAV	Q50hx9	tomato aspe
57	37	68.5	218	2	Q53HZ6_TAV	Q53hz6	tomato aspe
58	37	68.5	218	2	Q53HZ7_TAV	Q53hz7	tomato aspe
59	37	68.5	218	2	Q70DY7_9BROM	Q70dy7	cucumber mo
60	37	68.5	218	2	Q70G11_TAV	Q70g11	tomato aspe
61	37	68.5	218	2	Q80IH2_TAV	Q80ih2	tomato aspe
62	37	68.5	218	2	Q88619_TAV	Q88619	tomato aspe
63	37	68.5	219	2	Q3HVJ1_TAV	Q3hvj1	chrysanthem
64	37	68.5	226	1	RNC_BUCAI	P57346	buchnera ap
65	37	68.5	226	1	RNC_BUCAP	Q8k9r1	buchnera ap

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OM protein - protein search, using sw model

Run on: August 9, 2006, 06:40:12 ; Search time 92.9508 Seconds
(without alignments)
49.189 Million cell updates/sec

Title: US-10-661-366-7
Perfect score: 60
Sequence: 1 WIFPGDGSTK 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 837128

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Database : A_Geneseq_8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	60	100.0	10	9	ADY75172	Ady75172 Antibody
2	56	93.3	11	7	ABM78993	Abm78993 Monoclonal
3	56	93.3	11	8	ADP79655	Adp79655 8H9 Fv pr
4	40	66.7	10	9	AEA18654	Aea18654 Amino aci
5	39	65.0	9	8	ADN28280	Adn28280 Human CD3
6	36	60.0	8	9	AEA18653	Aea18653 Amino aci
7	35	58.3	10	9	ADW86101	Adw86101 Mouse DS6
8	34	56.7	13	8	ADM72620	Adm72620 Amino aci
9	34	56.7	15	9	ADZ80676	Adz80676 Amino aci
10	33	55.0	13	5	ADG67239	Adg67239 Human 5G1
11	33	55.0	13	5	ADG67238	Adg67238 Human 5G1
12	33	55.0	13	5	ADG67240	Adg67240 Human 5G1
13	33	55.0	13	8	ADM72619	Adm72619 Amino aci
14	33	55.0	15	2	AAAY40700	Aay40700 A3 deriva
15	33	55.0	15	3	AAAY93089	Aay93089 Transform
16	33	55.0	15	3	AAAY93088	Aay93088 Transform
17	33	55.0	15	3	AAB30039	Aab30039 Scaffold
18	32	53.3	8	10	AEE73476	Aee73476 Anti-Wnt2
19	32	53.3	13	5	ADG67237	Adg67237 Human 5G1
20	32	53.3	13	5	ADG67318	Adg67318 Human ant
21	32	53.3	13	5	ADG67316	Adg67316 Human ant
22	32	53.3	13	5	ADG67317	Adg67317 Human ant
23	32	53.3	13	8	ADM72628	Adm72628 Amino aci
24	32	53.3	13	8	ADM72626	Adm72626 Amino aci
25	32	53.3	13	8	ADM72627	Adm72627 Amino aci
26	32	53.3	14	8	ADR75422	Adr75422 Target mo
27	32	53.3	14	8	ADR75431	Adr75431 Target mo
28	32	53.3	14	8	ADR75423	Adr75423 Target mo
29	32	53.3	14	8	ADR75420	Adr75420 Target mo
30	32	53.3	14	8	ADR75425	Adr75425 Target mo
31	31.5	52.5	14	2	AAW72849	Aaw72849 Pyrococcu
32	31	51.7	10	4	AAG86561	Aag86561 Saccharom
33	31	51.7	14	4	AAG80095	Aag80095 Chemokine
34	31	51.7	15	7	ADC99264	Adc99264 Cancer-re
35	30	50.0	12	5	ABP56190	Abp56190 Chimeric
36	30	50.0	13	5	ABP56191	Abp56191 Chimeric
37	30	50.0	14	2	AAW01162	Aaw01162 Sorbitol
38	30	50.0	15	8	ADH77352	Adh77352 Yeast kil
39	29	48.3	10	2	AAR52539	Aar52539 Gloop-2 h
40	29	48.3	10	7	ADC99679	Adc99679 Potential
41	29	48.3	10	7	ADC99705	Adc99705 Cancer-re
42	29	48.3	10	9	AEB03794	Aeb03794 Murine 2E
43	29	48.3	11	8	ADU23528	Adu23528 Second an
44	29	48.3	13	8	ADO24017	Ado24017 HBV epito
45	29	48.3	13	9	ADZ40514	Adz40514 HBV EpiGe
46	28	46.7	8	8	ADU08085	Adu08085 Heat shoc
47	28	46.7	8	9	AEC16410	Aec16410 Glucose r
48	28	46.7	9	8	ADN63620	Adn63620 HLA bindi
49	28	46.7	10	5	AAU98285	Aau98285 M. tuberc
50	28	46.7	13	5	ADG67319	Adg67319 Human ant
51	28	46.7	13	7	ABU08852	Abu08852 Human gas
52	28	46.7	13	9	AEA14388	Aea14388 VEGF rela
53	28	46.7	14	4	AAB73656	Aab73656 Humanised
54	28	46.7	14	8	ADN11237	Adn11237 Peptide u
55	28	46.7	15	2	AAW18179	Aaw18179 Immunodom
56	28	46.7	15	2	AAW75628	Aaw75628 M. tuberc
57	28	46.7	15	2	AAW75627	Aaw75627 M. tuberc

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OM protein - protein search, using sw model

Run on: August 9, 2006, 07:02:53 ; Search time 24.5902 Seconds
(without alignments)
35.596 Million cell updates/sec

Title: US-10-661-366-7
Perfect score: 60
Sequence: 1 WIFPGDGSTK 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 249102

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Database : Issued_Patents_AA:*
1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	31.5	52.5	14	2	US-08-822-774-54	Sequence 54, Appl
2	31.5	52.5	14	2	US-09-632-711-54	Sequence 54, Appl

3	31.5	52.5	14	2	US-09-632-703B-54	Sequence 54, Appl
4	31.5	52.5	14	2	US-09-632-702-54	Sequence 54, Appl
5	31.5	52.5	14	2	US-09-399-003-54	Sequence 54, Appl
6	31.5	52.5	14	2	US-09-399-003-73	Sequence 73, Appl
7	30	50.0	14	1	US-08-809-860-5	Sequence 5, Appli
8	29	48.3	10	1	US-07-942-245-510	Sequence 510, App
9	28	46.7	12	7	5215909-3	Patent No. 5215909
10	28	46.7	14	2	US-09-889-480A-8	Sequence 8, Appli
11	28	46.7	15	2	US-09-157-689-77	Sequence 77, Appl
12	28	46.7	15	2	US-09-157-689-78	Sequence 78, Appl
13	28	46.7	15	2	US-09-953-510-77	Sequence 77, Appl
14	28	46.7	15	2	US-09-953-510-78	Sequence 78, Appl
15	28	46.7	15	3	US-09-953-413D-77	Sequence 77, Appl
16	28	46.7	15	3	US-09-953-413D-78	Sequence 78, Appl
17	27	45.0	7	2	US-09-870-472A-15	Sequence 15, Appl
18	27	45.0	11	2	US-09-224-785-27	Sequence 27, Appl
19	27	45.0	11	2	US-09-224-785-28	Sequence 28, Appl
20	27	45.0	11	2	US-09-224-785-29	Sequence 29, Appl
21	27	45.0	11	2	US-09-224-785-30	Sequence 30, Appl
22	27	45.0	11	2	US-09-756-594-27	Sequence 27, Appl
23	27	45.0	11	2	US-09-756-594-28	Sequence 28, Appl
24	27	45.0	11	2	US-09-756-594-29	Sequence 29, Appl
25	27	45.0	11	2	US-09-756-594-30	Sequence 30, Appl
26	27	45.0	15	1	US-08-665-220-26	Sequence 26, Appl
27	27	45.0	15	1	US-08-618-408B-26	Sequence 26, Appl
28	27	45.0	15	2	US-09-257-218-37	Sequence 37, Appl
29	27	45.0	15	2	US-09-311-760-37	Sequence 37, Appl
30	27	45.0	15	2	US-09-291-692-26	Sequence 26, Appl
31	27	45.0	15	2	US-09-561-756-75	Sequence 75, Appl
32	27	45.0	15	2	US-09-227-721-75	Sequence 75, Appl
33	27	45.0	15	2	US-08-865-579-37	Sequence 37, Appl
34	27	45.0	15	2	US-10-059-749-37	Sequence 37, Appl
35	27	45.0	15	2	US-09-954-697-75	Sequence 75, Appl
36	27	45.0	15	2	US-09-952-768-26	Sequence 26, Appl
37	27	45.0	15	2	US-10-668-955-26	Sequence 26, Appl
38	26	43.3	9	1	US-08-215-805A-16	Sequence 16, Appl
39	26	43.3	10	1	US-08-318-856A-15	Sequence 15, Appl
40	26	43.3	10	2	US-09-230-548-3	Sequence 3, Appli
41	26	43.3	11	2	US-09-224-785-5	Sequence 5, Appli
42	26	43.3	11	2	US-09-224-785-6	Sequence 6, Appli
43	26	43.3	11	2	US-09-756-594-5	Sequence 5, Appli
44	26	43.3	11	2	US-09-756-594-6	Sequence 6, Appli
45	26	43.3	12	1	US-08-260-582-47	Sequence 47, Appl
46	26	43.3	12	1	US-08-260-582-48	Sequence 48, Appl
47	26	43.3	12	2	US-09-224-785-4	Sequence 4, Appli
48	26	43.3	12	2	US-09-756-594-4	Sequence 4, Appli
49	26	43.3	12	5	PCT-US95-05471-47	Sequence 47, Appl
50	26	43.3	12	5	PCT-US95-05471-48	Sequence 48, Appl
51	26	43.3	13	2	US-09-763-397A-5	Sequence 5, Appli
52	26	43.3	14	2	US-08-946-329A-8	Sequence 8, Appli
53	26	43.3	14	2	US-08-567-357A-8	Sequence 8, Appli
54	26	43.3	14	2	US-08-729-743A-8	Sequence 8, Appli
55	26	43.3	14	2	US-08-349-498-8	Sequence 8, Appli
56	26	43.3	14	2	US-09-562-914-8	Sequence 8, Appli
57	26	43.3	14	5	PCT-US95-15463-8	Sequence 8, Appli
58	26	43.3	14	5	PCT-US95-15923-8	Sequence 8, Appli
59	26	43.3	15	1	US-08-056-200-22	Sequence 22, Appl
60	26	43.3	15	1	US-08-800-644-22	Sequence 22, Appl
61	26	43.3	15	2	US-10-034-974-30	Sequence 30, Appl
62	25	41.7	6	2	US-09-101-272G-69	Sequence 69, Appl
63	25	41.7	7	1	US-07-791-213D-34	Sequence 34, Appl

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OM protein - protein search, using sw model

Run on: August 9, 2006, 07:35:38 ; Search time 79.5082 Seconds
(without alignments)
58.260 Million cell updates/sec

Title: US-10-661-366-7
Perfect score: 60
Sequence: 1 WIFPGDGSTK 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 395127

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Database : Published Applications_AA_Main:*
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2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	60	100.0	10	5 US-10-661-366-7	Sequence 7, Appli

2	40	66.7	10	5	US-10-981-738-27	Sequence 27, Appl
3	39	65.0	9	4	US-10-428-335-80	Sequence 80, Appl
4	36	60.0	8	5	US-10-981-738-26	Sequence 26, Appl
5	35	58.3	10	5	US-10-895-135-21	Sequence 21, Appl
6	33	55.0	13	4	US-10-468-496-1730	Sequence 1730, Ap
7	33	55.0	13	4	US-10-468-496-1731	Sequence 1731, Ap
8	33	55.0	13	4	US-10-468-496-1732	Sequence 1732, Ap
9	32	53.3	8	6	US-11-131-425A-65	Sequence 65, Appl
10	32	53.3	13	4	US-10-468-496-1729	Sequence 1729, Ap
11	32	53.3	13	4	US-10-468-496-1808	Sequence 1808, Ap
12	32	53.3	13	4	US-10-468-496-1809	Sequence 1809, Ap
13	32	53.3	13	4	US-10-468-496-1810	Sequence 1810, Ap
14	31.5	52.5	14	5	US-10-738-917-54	Sequence 54, Appl
15	31.5	52.5	14	5	US-10-738-917-73	Sequence 73, Appl
16	31	51.7	14	4	US-10-239-423-51	Sequence 51, Appl
17	31	51.7	15	4	US-10-280-066-97	Sequence 97, Appl
18	30	50.0	12	4	US-10-059-261-285	Sequence 285, App
19	30	50.0	12	5	US-10-627-649-285	Sequence 285, App
20	29	48.3	10	4	US-10-280-066-517	Sequence 517, App
21	29	48.3	10	6	US-11-009-443-86	Sequence 86, Appl
22	29	48.3	12	5	US-10-901-011-100	Sequence 100, App
23	29	48.3	12	5	US-10-901-011-118	Sequence 118, App
24	28	46.7	8	4	US-10-367-580-197	Sequence 197, App
25	28	46.7	8	4	US-10-367-593-197	Sequence 197, App
26	28	46.7	8	4	US-10-367-594-197	Sequence 197, App
27	28	46.7	8	4	US-10-367-654-197	Sequence 197, App
28	28	46.7	8	4	US-10-367-658-197	Sequence 197, App
29	28	46.7	8	4	US-10-367-668-197	Sequence 197, App
30	28	46.7	8	4	US-10-367-674-197	Sequence 197, App
31	28	46.7	8	5	US-10-820-067A-176	Sequence 176, App
32	28	46.7	8	6	US-11-026-999-6	Sequence 6, Appli
33	28	46.7	9	5	US-10-530-061-220	Sequence 220, App
34	28	46.7	13	4	US-10-216-408-25	Sequence 25, Appl
35	28	46.7	13	4	US-10-468-496-1811	Sequence 1811, Ap
36	28	46.7	15	3	US-09-953-510-77	Sequence 77, Appl
37	28	46.7	15	3	US-09-953-510-78	Sequence 78, Appl
38	28	46.7	15	3	US-09-953-413-77	Sequence 77, Appl
39	28	46.7	15	3	US-09-953-413-78	Sequence 78, Appl
40	28	46.7	15	4	US-10-147-255-77	Sequence 77, Appl
41	28	46.7	15	4	US-10-147-255-78	Sequence 78, Appl
42	28	46.7	15	5	US-10-695-155-77	Sequence 77, Appl
43	28	46.7	15	5	US-10-695-155-78	Sequence 78, Appl
44	27	45.0	7	3	US-09-870-472-15	Sequence 15, Appl
45	27	45.0	8	5	US-10-950-163-129	Sequence 129, App
46	27	45.0	9	5	US-10-946-647-227	Sequence 227, App
47	27	45.0	9	5	US-10-946-647-1226	Sequence 1226, Ap
48	27	45.0	11	3	US-09-756-594-27	Sequence 27, Appl
49	27	45.0	11	3	US-09-756-594-28	Sequence 28, Appl
50	27	45.0	11	3	US-09-756-594-29	Sequence 29, Appl
51	27	45.0	11	3	US-09-756-594-30	Sequence 30, Appl
52	27	45.0	11	4	US-10-272-497-27	Sequence 27, Appl
53	27	45.0	11	4	US-10-272-497-28	Sequence 28, Appl
54	27	45.0	11	4	US-10-272-497-29	Sequence 29, Appl
55	27	45.0	11	4	US-10-272-497-30	Sequence 30, Appl
56	27	45.0	11	4	US-10-272-497-72	Sequence 72, Appl
57	27	45.0	11	4	US-10-272-497-74	Sequence 74, Appl
58	27	45.0	11	4	US-10-272-497-76	Sequence 76, Appl
59	27	45.0	11	4	US-10-272-497-79	Sequence 79, Appl
60	27	45.0	12	5	US-10-926-542-122	Sequence 122, App
61	27	45.0	13	3	US-09-272-975-20	Sequence 20, Appl
62	27	45.0	13	4	US-10-468-496-1728	Sequence 1728, Ap

SCORE Search Results Details for Application 10661366 and Search Result us-10-661-366-7.closed.rapbn.

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OM protein - protein search, using sw model

Run on: August 9, 2006, 07:36:48 ; Search time 12.623 Seconds
(without alignments)
53.325 Million cell updates/sec

Title: US-10-661-366-7
Perfect score: 60
Sequence: 1 WIFPGDGSTK 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 239914 seqs, 67312017 residues

Total number of hits satisfying chosen parameters: 27373

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Database : Published_Applications_AA_New:*
1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
8: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	% Query
--------	------------

No.	Score	Match Length	DB	ID	Description	
1	36	60.0	11	7	US-11-242-617-10	Sequence 10, Appl
2	36	60.0	11	7	US-11-242-617-43	Sequence 43, Appl
3	34	56.7	11	7	US-11-242-617-31	Sequence 31, Appl
4	31	51.7	11	7	US-11-242-617-40	Sequence 40, Appl
5	29	48.3	11	7	US-11-242-617-19	Sequence 19, Appl
6	27	45.0	11	6	US-10-540-431-9	Sequence 9, Appli
7	26	43.3	11	7	US-11-061-841-340	Sequence 340, App
8	26	43.3	12	7	US-11-045-488-34	Sequence 34, Appl
9	25	41.7	11	7	US-11-242-617-13	Sequence 13, App
10	25	41.7	11	7	US-11-242-617-16	Sequence 16, Appl
11	25	41.7	11	7	US-11-242-617-28	Sequence 28, Appl
12	25	41.7	12	6	US-10-953-613C-485	Sequence 485, App
13	25	41.7	12	7	US-11-099-283B-435	Sequence 435, App
14	25	41.7	12	7	US-11-234-731-46	Sequence 46, Appl
15	24	40.0	9	7	US-11-140-487A-284	Sequence 284, App
16	24	40.0	9	7	US-11-140-487A-407	Sequence 407, App
17	24	40.0	9	7	US-11-140-487A-519	Sequence 519, App
18	24	40.0	9	7	US-11-140-487A-608	Sequence 608, App
19	24	40.0	9	7	US-11-140-487A-683	Sequence 683, App
20	24	40.0	10	7	US-11-140-487A-990	Sequence 990, App
21	24	40.0	10	7	US-11-140-487A-1077	Sequence 1077, Ap
22	24	40.0	10	7	US-11-140-487A-1321	Sequence 1321, Ap
23	24	40.0	10	7	US-11-140-487A-1920	Sequence 1920, Ap
24	24	40.0	11	7	US-11-242-617-34	Sequence 34, Appl
25	24	40.0	13	6	US-10-991-309B-70	Sequence 70, Appl
26	24	40.0	14	7	US-11-094-132-27	Sequence 27, Appl
27	24	40.0	15	7	US-11-240-937-4	Sequence 4, Appli
28	23.5	39.2	15	7	US-11-295-192A-131	Sequence 131, App
29	23.5	39.2	15	7	US-11-295-192A-132	Sequence 132, App
30	23.5	39.2	15	7	US-11-295-192A-133	Sequence 133, App
31	23.5	39.2	15	7	US-11-295-192A-134	Sequence 134, App
32	23.5	39.2	15	7	US-11-295-192A-135	Sequence 135, App
33	23.5	39.2	15	7	US-11-295-192A-136	Sequence 136, App
34	23.5	39.2	15	7	US-11-295-192A-137	Sequence 137, App
35	23.5	39.2	15	7	US-11-295-192A-138	Sequence 138, App
36	23.5	39.2	15	7	US-11-295-192A-139	Sequence 139, App
37	23.5	39.2	15	7	US-11-295-192A-140	Sequence 140, App
38	23	38.3	7	6	US-10-533-701-12	Sequence 12, Appl
39	23	38.3	7	7	US-11-183-325-6	Sequence 6, Appli
40	23	38.3	9	7	US-11-140-487A-1162	Sequence 1162, Ap
41	23	38.3	9	7	US-11-183-325-5	Sequence 5, Appli
42	23	38.3	9	7	US-11-183-325-25	Sequence 25, Appl
43	23	38.3	10	7	US-11-140-487A-1163	Sequence 1163, Ap
44	23	38.3	10	7	US-11-183-325-2	Sequence 2, Appli
45	23	38.3	11	6	US-10-540-431-3	Sequence 3, Appli
46	23	38.3	12	6	US-10-531-701-14	Sequence 14, Appl
47	23	38.3	14	6	US-10-821-930-20	Sequence 20, Appl
48	23	38.3	14	7	US-11-290-639A-35	Sequence 35, Appl
49	23	38.3	14	7	US-11-290-639A-37	Sequence 37, Appl
50	22	36.7	8	6	US-10-544-048-3	Sequence 3, Appli
51	22	36.7	8	6	US-10-544-048-4	Sequence 4, Appli
52	22	36.7	9	6	US-10-521-140-29	Sequence 29, Appl
53	22	36.7	9	7	US-11-223-610-168	Sequence 168, App
54	22	36.7	9	7	US-11-223-610-169	Sequence 169, App
55	22	36.7	10	6	US-10-529-452-3	Sequence 3, Appli
56	22	36.7	10	7	US-11-134-871-3559	Sequence 3559, Ap
57	22	36.7	10	7	US-11-373-754-16	Sequence 16, Appl
58	22	36.7	11	6	US-10-570-220-24	Sequence 24, Appl
59	22	36.7	12	7	US-11-177-358C-16	Sequence 16, Appl

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OM protein - protein search, using sw model

Run on: August 9, 2006, 06:51:47 ; Search time 13.7705 Seconds
(without alignments)
69.872 Million cell updates/sec

Title: US-10-661-366-7
Perfect score: 60
Sequence: 1 WIFPGDGSTK 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 2523

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Database : PIR_80:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	25	41.7	13	2	A46463	preabsorbing antig
2	22	36.7	9	2	A37027	macrophage chemota
3	22	36.7	9	2	S10784	enamelin i - bovin
4	22	36.7	10	2	PT0289	Ig heavy chain CRD
5	22	36.7	12	2	S70337	napin small chain
6	22	36.7	12	2	PH1324	Ig heavy chain DJ
7	20	33.3	8	2	A46306	spasmogenic toxin
8	20	33.3	12	1	JTJG0	tremerogen A-10 -

9	20	33.3	13	2	B26406	Ig kappa chain J r
10	20	33.3	13	2	A47630	Ig kappa chain J r
11	20	33.3	14	2	PH1322	Ig heavy chain DJ
12	20	33.3	14	2	E49039	T-cell receptor be
13	19	31.7	6	2	A61049	halo-toxin - Pseud
14	19	31.7	7	2	PT0689	T-cell receptor be
15	19	31.7	9	2	B20569	serum amyloid P-co
16	19	31.7	10	2	S71948	matrix metalloprot
17	19	31.7	10	2	T17054	cytochrome-c oxida
18	19	31.7	10	2	T17063	cytochrome-c oxida
19	19	31.7	10	2	T12325	cytochrome-c oxida
20	19	31.7	10	2	T12329	cytochrome-c oxida
21	19	31.7	10	2	T14215	cytochrome-c oxida
22	19	31.7	10	2	T14223	cytochrome-c oxida
23	19	31.7	11	2	S78026	ribosomal protein
24	19	31.7	11	2	S07207	Crinia-angiotensin
25	19	31.7	12	2	C39109	hypothetical 1.2K
26	19	31.7	12	2	B46662	collagen alpha 2(V
27	19	31.7	13	2	PH0756	T-cell receptor be
28	19	31.7	14	2	PA0096	pyruvate decarboxy
29	19	31.7	14	2	S33802	chaperone, TCP1-re
30	19	31.7	15	2	C44101	calmodulin, vasoac
31	19	31.7	15	2	C56979	collagen alpha 1(I
32	19	31.7	15	2	H56978	collagen alpha 1(X
33	18	30.0	5	2	PT0703	T-cell receptor be
34	18	30.0	6	2	PT0604	T-cell receptor be
35	18	30.0	7	2	E61491	seed protein ws-5
36	18	30.0	7	2	PT0543	T-cell receptor be
37	18	30.0	8	2	PT0279	Ig heavy chain CRD
38	18	30.0	8	2	PT0725	T-cell receptor be
39	18	30.0	8	2	A61328	trypsin (EC 3.4.21
40	18	30.0	10	2	PQ0753	beta-fructofuranos
41	18	30.0	13	1	XAVI9B	angiotensin-conver
42	18	30.0	14	2	S17766	beta-glucosidase (
43	18	30.0	14	2	PH0795	T-cell receptor al
44	18	30.0	14	2	A60158	disaggregatase - M
45	18	30.0	14	2	S33801	chaperone, TCP1-re
46	18	30.0	15	2	B33208	calreticulin, uter
47	18	30.0	15	2	PA0058	protein QF200022 -
48	18	30.0	15	2	C61511	milk band B protei
49	18	30.0	15	2	S05700	insulin-like growt
50	18	30.0	15	2	AF0832	phe leader peptide
51	18	30.0	15	2	PH0216	agarase (EC 3.2.1.
52	18	30.0	15	2	S05699	insulin-like growt
53	17	28.3	7	2	A44428	platelet aggregati
54	17	28.3	7	2	PT0544	T-cell receptor be
55	17	28.3	8	2	PT0631	T-cell receptor be
56	17	28.3	8	2	T13818	cytochrome oxidase
57	17	28.3	9	2	PT0324	Ig heavy chain CRD
58	17	28.3	10	2	A37268	Ig heavy chain C r
59	17	28.3	10	2	T13976	cytochrome-c oxida
60	17	28.3	10	2	T17057	cytochrome-c oxida
61	17	28.3	10	2	T12303	cytochrome-c oxida
62	17	28.3	10	2	T14019	cytochrome-c oxida
63	17	28.3	10	2	T17060	cytochrome-c oxida
64	17	28.3	10	2	T14043	cytochrome-c oxida
65	17	28.3	10	2	T14054	cytochrome-c oxida
66	17	28.3	10	2	T17066	cytochrome-c oxida
67	17	28.3	10	2	T17069	cytochrome-c oxida
68	17	28.3	10	2	T12308	cytochrome-c oxida
69	17	28.3	10	2	T17072	cytochrome-c oxida

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OM protein - protein search, using sw model

Run on: August 9, 2006, 06:40:52 ; Search time 111.475 Seconds
(without alignments)
82.979 Million cell updates/sec

Title: US-10-661-366-7
Perfect score: 60
Sequence: 1 WIFPGDGSTK 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 8966

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Database : UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	30	50.0	15	2	Q42223_ARATH	Q42223 arabidopsis
2	27	45.0	15	2	Q9UCJ8_HUMAN	Q9ucj8 homo sapien
3	26	43.3	15	1	CWP14_PHAVU	P80773 phaseolus v
4	25	41.7	13	2	Q9R5L4_9STRE	Q9r5l4 streptococc

5	22	36.7	9	2	Q7M4S2_HUMAN	Q7m4s2	homo sapien
6	22	36.7	9	2	Q7M2M7_BOVIN	Q7m2m7	bos taurus
7	22	36.7	13	2	Q9UDC6_HUMAN	Q9udc6	homo sapien
8	22	36.7	14	2	Q9QVD9_9MURI	Q9qvd9	rattus sp.
9	21	35.0	9	1	UPA6_HUMAN	P30092	homo sapien
10	21	35.0	9	2	Q8IUJ5_HUMAN	Q8iuj5	homo sapien
11	21	35.0	10	2	Q9R5N2_CLOBO	Q9r5n2	clostridium
12	21	35.0	12	1	LICA_BACSU	P83878	bacillus su
13	21	35.0	12	2	Q3V793_HUMAN	Q3v793	homo sapien
14	21	35.0	13	1	IDH3A_CANFA	P54836	canis famil
15	20.5	34.2	10	2	Q7Z5A2_HUMAN	Q7z5a2	homo sapien
16	20	33.3	8	1	TXV1_PHONI	Q7m3pl	phoneutria
17	20	33.3	10	2	Q6LA62_HUMAN	Q6la62	homo sapien
18	20	33.3	10	2	Q599W9_MOUSE	Q599w9	mus musculu
19	20	33.3	10	2	Q7ZZJ2_MOTFL	Q7zzj2	motacilla f
20	20	33.3	11	2	Q8KTN1_TREPR	Q8ktn1	tremblaya p
21	20	33.3	11	2	Q7ZZI6_MOTFL	Q7zzi6	motacilla f
22	20	33.3	11	2	Q7ZZI9_MOTFL	Q7zzi9	motacilla f
23	20	33.3	11	2	Q800X7_CHESE	Q800x7	chelydra se
24	20	33.3	12	1	TA10_TREME	P01371	tremella me
25	20	33.3	12	2	Q61331_MOUSE	Q61331	mus musculu
26	20	33.3	12	2	Q7ZZI3_MOTFL	Q7zzi3	motacilla f
27	20	33.3	13	2	Q7ZT28_MOTFL	Q7zt28	motacilla f
28	20	33.3	13	2	Q7ZT29_MOTCT	Q7zt29	motacilla c
29	20	33.3	13	2	Q7ZZI4_MOTFL	Q7zzi4	motacilla f
30	20	33.3	13	2	Q7ZZI5_MOTFL	Q7zzi5	motacilla f
31	20	33.3	13	2	Q7ZZI7_MOTFL	Q7zzi7	motacilla f
32	20	33.3	13	2	Q7ZZI8_MOTFL	Q7zzi8	motacilla f
33	20	33.3	13	2	Q7ZZJ0_MOTFL	Q7zzj0	motacilla f
34	20	33.3	13	2	Q7ZZJ1_MOTFL	Q7zzj1	motacilla f
35	20	33.3	13	2	Q7ZZJ3_MOTFL	Q7zzj3	motacilla f
36	20	33.3	13	2	Q7ZZJ4_MOTCT	Q7zzj4	motacilla c
37	20	33.3	13	2	Q7ZZJ5_MOTCI	Q7zzj5	motacilla c
38	20	33.3	13	2	Q7ZZJ6_9PASS	Q7zzj6	anthus prat
39	20	33.3	14	2	Q3TU57_MOUSE	Q3tu57	mus musculu
40	20	33.3	15	2	Q9UCB9_HUMAN	Q9ucb9	homo sapien
41	20	33.3	15	2	Q9TR45_BOVIN	Q9tr45	bos taurus
42	20	33.3	15	2	Q8SL36_9MAGN	Q8sl36	monanthes i
43	19	31.7	7	1	CWP17_LYCES	P80813	lycopersico
44	19	31.7	7	1	PPH2_LYCES	P83379	lycopersico
45	19	31.7	8	2	Q7GEM6_BRALA	Q7gem6	branchiosto
46	19	31.7	8	2	Q8WGD7_9EUCA	Q8wgd7	lomis hirta
47	19	31.7	8	2	Q32XK9_PLEA	Q32xk9	plecotus ra
48	19	31.7	8	2	Q9TT78_CANFA	Q9tt78	canis famil
49	19	31.7	8	2	Q3ZDX7_9SMEG	Q3zdx7	kryptolebia
50	19	31.7	8	2	Q3ZDX9_RIVMA	Q3zdx9	rivulus mar
51	19	31.7	8	2	Q3ZDY5_9SMEG	Q3zdy5	kryptolebia
52	19	31.7	8	2	Q7I5L5_VARDU	Q7i5l5	varanus dum
53	19	31.7	8	2	Q94V88_9SAUR	Q94v88	varanus tri
54	19	31.7	8	2	Q94V91_VARTI	Q94v91	varanus tim
55	19	31.7	8	2	Q94VE4_VARML	Q94ve4	varanus mel
56	19	31.7	8	2	Q94VF9_VARIN	Q94vf9	varanus ind
57	19	31.7	8	2	Q94VJ4_VARBN	Q94vj4	varanus ben
58	19	31.7	9	1	SAMP_MUSCA	P19095	mustelus ca
59	19	31.7	9	2	Q8WGE6_PROCL	Q8wge6	procambarus
60	19	31.7	9	2	Q71DX2_9SAUR	Q7ldx2	urostrophus
61	19	31.7	9	2	Q94VD8_VARNI	Q94vd8	varanus nil
62	19	31.7	9	2	Q94VE1_VARME	Q94ve1	varanus mer
63	19	31.7	9	2	Q94VH4_9SAUR	Q94vh4	varanus gla
64	19	31.7	9	2	Q94VI8_VARER	Q94vi8	varanus ere
65	19	31.7	9	2	Q94VJ1_VARDO	Q94vj1	varanus dor

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OM protein - protein search, using sw model

Run on: August 9, 2006, 07:45:18 ; Search time 25.256 Seconds
 (without alignments)
 181.033 Million cell updates/sec

Title: US-10-661-366-7
 Perfect score: 60
 Sequence: 1 WIFPGDGSTK 10

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 1000 summaries

Database : A_Geneseq_8:*
 1: geneseqp1980s:*
 2: geneseqp1990s:*
 3: geneseqp2000s:*
 4: geneseqp2001s:*
 5: geneseqp2002s:*
 6: geneseqp2003as:*
 7: geneseqp2003bs:*
 8: geneseqp2004s:*
 9: geneseqp2005s:*
 10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	60	100.0	10	9	ADY75172	Ady75172 Antibody
2	60	100.0	17	6	ABJ18551	Abj18551 Gangliosi
3	60	100.0	119	6	ABJ18572	Abj18572 Gangliosi
4	60	100.0	119	6	ABJ18570	Abj18570 Gangliosi
5	60	100.0	125	9	ADY75166	Ady75166 Antibody
6	60	100.0	555	4	AAB19871	Aab19871 Activatin
7	60	100.0	565	4	AAB19873	Aab19873 Activatin
8	60	100.0	577	4	AAB19872	Aab19872 Activatin
9	60	100.0	704	4	AAB19888	Aab19888 MLV envel
10	57	95.0	17	8	ADO60472	Ado60472 Mouse ant
11	57	95.0	17	9	ADZ45483	Adz45483 Murine fa
12	57	95.0	17	9	AEB24624	Aeb24624 Humanized
13	57	95.0	113	8	ADO60449	Ado60449 Humanised
14	57	95.0	113	8	ADO60448	Ado60448 Humanised
15	57	95.0	113	8	ADO60444	Ado60444 Humanised
16	57	95.0	113	8	ADO60442	Ado60442 Mouse ant
17	57	95.0	113	8	ADO60450	Ado60450 Humanised
18	57	95.0	113	8	ADO60447	Ado60447 Humanised
19	57	95.0	113	8	ADO60446	Ado60446 Humanised
20	57	95.0	113	9	AEB24594	Aeb24594 Murine MA
21	57	95.0	113	9	AEB24596	Aeb24596 Humanized
22	57	95.0	113	9	AEB24602	Aeb24602 Humanized
23	57	95.0	113	9	AEB24600	Aeb24600 Humanized
24	57	95.0	113	9	AEB24598	Aeb24598 Humanized
25	57	95.0	113	9	AEB24599	Aeb24599 Humanized
26	57	95.0	113	9	AEB24601	Aeb24601 Humanized
27	57	95.0	115	9	ADZ45481	Adz45481 Murine fa
28	57	95.0	116	2	AAR79241	Aar79241 Heavy cha
29	57	95.0	138	8	ADI26639	Adi26639 Mouse ant
30	57	95.0	269	8	ADR28054	Adr28054 NPB polyp
31	56	93.3	11	7	ABM78993	Abm78993 Monoclonal
32	56	93.3	11	8	ADP79655	Adp79655 8H9 Fv pr
33	56	93.3	118	8	ADP79643	Adp79643 8H9 VH. 1
34	56	93.3	243	7	ABM78999	Abm78999 Monoclonal
35	56	93.3	243	7	ABM78998	Abm78998 Monoclonal
36	56	93.3	243	8	ADP79639	Adp79639 8H9 scFv
37	56	93.3	243	8	ADP79638	Adp79638 8H9 scFv.
38	55	91.7	118	3	AAB11391	Aab11391 Murine II
39	52	86.7	20	5	AAU70773	Aau70773 Hepatitis
40	52	86.7	20	7	ADC85027	Adc85027 HBV HBcAg
41	52	86.7	20	8	ADK14584	Adk14584 Hepatitis
42	52	86.7	20	10	AEF35687	Aef35687 Hepatitis
43	52	86.7	112	4	AAB74000	Aab74000 Anti-chry
44	52	86.7	118	7	ADP43262	Adp43262 Antibody
45	52	86.7	118	8	ADN62628	Adn62628 HIV gp 41
46	52	86.7	118	8	ADN62634	Adn62634 HIV gp 41
47	52	86.7	119	5	AAU70766	Aau70766 Hepatitis
48	52	86.7	119	6	AAE33325	Aae33325 12E antib
49	52	86.7	119	6	AAE33327	Aae33327 3D antibo
50	52	86.7	119	7	ADC85020	Adc85020 HBV HBcAg
51	52	86.7	119	8	ADK14577	Adk14577 Hepatitis
52	52	86.7	119	8	ADN36310	Adn36310 Rat anti-
53	52	86.7	119	9	ADZ21523	Adz21523 Anti-Muc-
54	52	86.7	119	9	ADZ21525	Adz21525 Anti-Muc-
55	52	86.7	119	10	AEF35680	Aef35680 HBV-speci
56	52	86.7	194	6	AAE33334	Aae33334 3D antibo
57	52	86.7	194	9	ADZ21538	Adz21538 Anti-Muc-

SCORE Search Results Details for Application 10661366 and Search Result us-10-661-366-7.1

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OM protein - protein search, using sw model

Run on: August 9, 2006, 08:17:00 ; Search time 6.58703 Seconds
(without alignments)
132.883 Million cell updates/sec

Title: US-10-661-366-7
Perfect score: 60
Sequence: 1 WIFPGDGSTK 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Issued_Patents_AA:*
1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	57	95.0	116	1	US-08-888-366-2	Sequence 2, Appli
2	52	86.7	20	2	US-09-556-605-8	Sequence 8, Appli

3	52	86.7	119	2	US-09-556-605-1	Sequence 1, Appli
4	43	71.7	1688	2	US-10-042-665A-7	Sequence 7, Appli
5	43	71.7	4572	2	US-10-042-665A-4	Sequence 4, Appli
6	43	71.7	5069	2	US-10-042-665A-5	Sequence 5, Appli
7	42	70.0	17	2	US-09-269-921-7	Sequence 7, Appli
8	42	70.0	138	2	US-08-603-024-2	Sequence 2, Appli
9	42	70.0	139	1	US-08-253-877C-8	Sequence 8, Appli
10	42	70.0	139	1	US-08-253-877C-19	Sequence 19, Appl
11	42	70.0	139	1	US-08-452-164A-8	Sequence 8, Appli
12	42	70.0	139	1	US-08-452-164A-19	Sequence 19, Appl
13	42	70.0	139	2	US-08-603-024-18	Sequence 18, Appl
14	42	70.0	139	2	US-09-355-925-7	Sequence 7, Appli
15	42	70.0	139	2	US-09-355-925-8	Sequence 8, Appli
16	42	70.0	139	2	US-08-450-809-14	Sequence 14, Appl
17	42	70.0	139	2	US-09-269-921-105	Sequence 105, App
18	42	70.0	139	2	US-09-269-921-108	Sequence 108, App
19	42	70.0	139	2	US-09-269-921-109	Sequence 109, App
20	42	70.0	139	2	US-09-269-921-110	Sequence 110, App
21	42	70.0	139	2	US-09-269-921-111	Sequence 111, App
22	42	70.0	139	2	US-09-269-921-112	Sequence 112, App
23	42	70.0	139	2	US-09-269-921-113	Sequence 113, App
24	42	70.0	139	2	US-09-269-921-114	Sequence 114, App
25	42	70.0	139	2	US-09-269-921-115	Sequence 115, App
26	42	70.0	139	2	US-09-269-921-116	Sequence 116, App
27	42	70.0	139	2	US-09-269-921-117	Sequence 117, App
28	42	70.0	139	2	US-09-269-921-118	Sequence 118, App
29	42	70.0	139	2	US-09-269-921-119	Sequence 119, App
30	42	70.0	139	2	US-09-269-921-120	Sequence 120, App
31	42	70.0	139	2	US-09-269-921-121	Sequence 121, App
32	42	70.0	139	2	US-09-269-921-122	Sequence 122, App
33	42	70.0	139	2	US-09-269-921-123	Sequence 123, App
34	42	70.0	139	2	US-09-269-921-124	Sequence 124, App
35	42	70.0	139	2	US-09-269-921-125	Sequence 125, App
36	42	70.0	139	2	US-09-269-921-126	Sequence 126, App
37	42	70.0	139	2	US-09-269-921-127	Sequence 127, App
38	42	70.0	139	2	US-09-269-921-128	Sequence 128, App
39	42	70.0	249	1	US-08-797-689-18	Sequence 18, Appl
40	42	70.0	249	2	US-09-984-186-18	Sequence 18, Appl
41	42	70.0	249	2	US-10-237-866-18	Sequence 18, Appl
42	42	70.0	249	2	US-10-702-636-18	Sequence 18, Appl
43	42	70.0	249	2	US-10-702-536-18	Sequence 18, Appl
44	42	70.0	364	2	US-08-896-537A-3	Sequence 3, Appli
45	41	68.3	122	2	US-08-767-128-4	Sequence 4, Appli
46	40	66.7	1721	2	US-10-042-665A-6	Sequence 6, Appli
47	40	66.7	1875	2	US-10-042-665A-2	Sequence 2, Appli
48	40	66.7	3413	2	US-10-042-665A-8	Sequence 8, Appli
49	39	65.0	17	1	US-08-318-970B-7	Sequence 7, Appli
50	39	65.0	17	1	US-08-482-228-40	Sequence 40, Appl
51	39	65.0	17	1	US-08-182-067-14	Sequence 14, Appl
52	39	65.0	17	1	US-08-465-313-14	Sequence 14, Appl
53	39	65.0	17	2	US-08-482-528-40	Sequence 40, Appl
54	39	65.0	17	2	US-09-809-739-7	Sequence 7, Appli
55	39	65.0	17	2	US-09-378-967-14	Sequence 14, Appl
56	39	65.0	134	1	US-08-137-117D-39	Sequence 39, Appl
57	39	65.0	134	1	US-08-436-717-39	Sequence 39, Appl
58	39	65.0	139	1	US-08-039-198B-10	Sequence 10, Appl
59	39	65.0	139	1	US-08-182-067-10	Sequence 10, Appl
60	39	65.0	139	1	US-08-465-313-10	Sequence 10, Appl
61	39	65.0	139	2	US-09-809-739-5	Sequence 5, Appli
62	39	65.0	139	2	US-09-809-739-9	Sequence 9, Appli
63	39	65.0	139	2	US-09-378-967-10	Sequence 10, Appl

SCORE Search Results Details for Application 10661366 and Search Result us-10-661-366-7.ra

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OM protein - protein search, using sw model

Run on: August 9, 2006, 09:01:05 ; Search time 21.3993 Seconds
(without alignments)
216.462 Million cell updates/sec

Title: US-10-661-366-7
Perfect score: 60
Sequence: 1 WIFPGDGSTK 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Published_Applications_AA_Main:*
1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	60	100.0	10	5	US-10-661-366-7	Sequence 7, Appli
2	60	100.0	17	5	US-10-473-977-16	Sequence 16, Appl
3	60	100.0	119	5	US-10-473-977-67	Sequence 67, Appl

4	60	100.0	125	5	US-10-661-366-1	Sequence 1, Appli
5	57	95.0	17	4	US-10-307-276B-33	Sequence 33, Appl
6	57	95.0	17	6	US-11-061-956-33	Sequence 33, Appl
7	57	95.0	113	4	US-10-307-276B-3	Sequence 3, Appli
8	57	95.0	113	4	US-10-307-276B-5	Sequence 5, Appli
9	57	95.0	113	4	US-10-307-276B-7	Sequence 7, Appli
10	57	95.0	113	4	US-10-307-276B-8	Sequence 8, Appli
11	57	95.0	113	4	US-10-307-276B-9	Sequence 9, Appli
12	57	95.0	113	4	US-10-307-276B-10	Sequence 10, Appl
13	57	95.0	113	4	US-10-307-276B-11	Sequence 11, Appl
14	57	95.0	113	6	US-11-061-956-3	Sequence 3, Appli
15	57	95.0	113	6	US-11-061-956-5	Sequence 5, Appli
16	57	95.0	113	6	US-11-061-956-7	Sequence 7, Appli
17	57	95.0	113	6	US-11-061-956-8	Sequence 8, Appli
18	57	95.0	113	6	US-11-061-956-9	Sequence 9, Appli
19	57	95.0	113	6	US-11-061-956-10	Sequence 10, Appl
20	57	95.0	113	6	US-11-061-956-11	Sequence 11, Appl
21	57	95.0	138	2	US-08-779-784-31	Sequence 31, Appl
22	57	95.0	138	4	US-10-010-729-67	Sequence 67, Appl
23	56	93.3	118	5	US-10-537-061-7	Sequence 7, Appli
24	56	93.3	243	4	US-10-097-558-2	Sequence 2, Appli
25	56	93.3	243	4	US-10-097-558-3	Sequence 3, Appli
26	56	93.3	243	5	US-10-505-658-2	Sequence 2, Appli
27	56	93.3	243	5	US-10-505-658-3	Sequence 3, Appli
28	56	93.3	243	5	US-10-537-061-2	Sequence 2, Appli
29	56	93.3	243	5	US-10-537-061-3	Sequence 3, Appli
30	55	91.7	118	3	US-09-926-323-2	Sequence 2, Appli
31	52	86.7	17	6	US-11-130-206-31	Sequence 31, Appl
32	52	86.7	17	6	US-11-130-206-39	Sequence 39, Appl
33	52	86.7	20	3	US-09-839-447A-8	Sequence 8, Appli
34	52	86.7	20	4	US-10-153-271-8	Sequence 8, Appli
35	52	86.7	20	4	US-10-369-060A-8	Sequence 8, Appli
36	52	86.7	20	6	US-11-188-187A-8	Sequence 8, Appli
37	52	86.7	119	3	US-09-839-447A-1	Sequence 1, Appli
38	52	86.7	119	4	US-10-112-788-1	Sequence 1, Appli
39	52	86.7	119	4	US-10-112-788-3	Sequence 3, Appli
40	52	86.7	119	4	US-10-153-271-1	Sequence 1, Appli
41	52	86.7	119	4	US-10-369-060A-1	Sequence 1, Appli
42	52	86.7	119	4	US-10-435-614-1	Sequence 1, Appli
43	52	86.7	119	4	US-10-435-614-3	Sequence 3, Appli
44	52	86.7	119	4	US-10-689-921-5	Sequence 5, Appli
45	52	86.7	119	6	US-11-188-187A-1	Sequence 1, Appli
46	52	86.7	194	4	US-10-112-788-10	Sequence 10, Appl
47	52	86.7	194	4	US-10-435-614-16	Sequence 16, Appl
48	52	86.7	241	5	US-10-902-546-5	Sequence 5, Appli
49	52	86.7	241	5	US-10-902-546-6	Sequence 6, Appli
50	52	86.7	246	5	US-10-861-617-15	Sequence 15, Appl
51	52	86.7	246	5	US-10-861-617-17	Sequence 17, Appl
52	52	86.7	261	4	US-10-689-921-7	Sequence 7, Appli
53	52	86.7	281	4	US-10-112-788-9	Sequence 9, Appli
54	52	86.7	281	4	US-10-435-614-15	Sequence 15, Appl
55	49	81.7	17	6	US-11-036-098-10	Sequence 10, Appl
56	49	81.7	17	6	US-11-226-886-39	Sequence 39, Appl
57	49	81.7	17	6	US-11-159-046-22	Sequence 22, Appl
58	49	81.7	103	5	US-10-683-547-15	Sequence 15, Appl
59	49	81.7	117	5	US-10-683-547-14	Sequence 14, Appl
60	49	81.7	118	5	US-10-683-547-12	Sequence 12, Appl
61	49	81.7	118	5	US-10-507-662-32	Sequence 32, Appl
62	49	81.7	118	5	US-10-507-662-33	Sequence 33, Appl
63	49	81.7	119	6	US-11-226-886-46	Sequence 46, Appl
64	49	81.7	119	6	US-11-159-046-12	Sequence 12, Appl

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Score Home	Retrieve Application	SCORE System	SCORE	Comments /
Page	List	Overview	FAQ	Suggestions

This page gives you Search Results detail for the Application 10661366 and Search Result us-10-661-366-7.rapbn.

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OM protein - protein search, using sw model

Run on: August 9, 2006, 09:02:15 ; Search time 3.27645 Seconds
(without alignments)
205.442 Million cell updates/sec

Title: US-10-661-366-7
Perfect score: 60
Sequence: 1 WIFPGDGSTK 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 239914 seqs, 67312017 residues

Total number of hits satisfying chosen parameters: 239914

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Published_Applications_AA_New:*

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- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	% Query
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No.	Score	Match	Length	DB	ID	Description
1	57	95.0	138	7	US-11-224-664-31	Sequence 31, Appl
2	57	95.0	269	6	US-10-539-402-1	Sequence 1, Appli
3	49	81.7	103	6	US-10-684-237-15	Sequence 15, Appl
4	49	81.7	117	6	US-10-684-237-14	Sequence 14, Appl
5	49	81.7	118	6	US-10-684-237-12	Sequence 12, Appl
6	48	80.0	117	7	US-11-256-060-8	Sequence 8, Appli
7	48	80.0	117	7	US-11-290-687-68	Sequence 68, Appl
8	48	80.0	447	7	US-11-256-060-19	Sequence 19, Appl
9	47	78.3	298	7	US-11-330-403-5386	Sequence 5386, Ap
10	47	78.3	298	7	US-11-330-403-13810	Sequence 13810, A
11	47	78.3	298	7	US-11-330-403-17212	Sequence 17212, A
12	47	78.3	322	7	US-11-330-403-17966	Sequence 17966, A
13	44	73.3	167	7	US-11-301-373-56	Sequence 56, Appl
14	44	73.3	295	7	US-11-330-403-5764	Sequence 5764, Ap
15	44	73.3	347	7	US-11-330-403-3133	Sequence 3133, Ap
16	44	73.3	351	7	US-11-330-403-514	Sequence 514, App
17	43	71.7	291	7	US-11-330-403-8108	Sequence 8108, Ap
18	43	71.7	292	7	US-11-330-403-5100	Sequence 5100, Ap
19	43	71.7	292	7	US-11-330-403-11924	Sequence 11924, A
20	43	71.7	293	7	US-11-330-403-8469	Sequence 8469, Ap
21	43	71.7	293	7	US-11-330-403-9770	Sequence 9770, Ap
22	43	71.7	294	7	US-11-330-403-9838	Sequence 9838, Ap
23	43	71.7	298	7	US-11-330-403-5070	Sequence 5070, Ap
24	43	71.7	311	7	US-11-330-403-5013	Sequence 5013, Ap
25	42	70.0	120	7	US-11-290-687-70	Sequence 70, Appl
26	42	70.0	139	6	US-10-533-104A-21	Sequence 21, Appl
27	42	70.0	139	6	US-10-533-104A-22	Sequence 22, Appl
28	42	70.0	249	7	US-11-330-353-18	Sequence 18, Appl
29	42	70.0	298	7	US-11-330-403-462	Sequence 462, App
30	42	70.0	364	6	US-10-511-937-2927	Sequence 2927, Ap
31	42	70.0	364	7	US-11-246-999-92	Sequence 92, Appl
32	42	70.0	375	6	US-10-449-902-50898	Sequence 50898, A
33	42	70.0	519	7	US-11-330-403-6792	Sequence 6792, Ap
34	42	70.0	542	6	US-10-449-902-34673	Sequence 34673, A
35	42	70.0	610	6	US-10-449-902-45664	Sequence 45664, A
36	42	70.0	610	6	US-10-449-902-48612	Sequence 48612, A
37	42	70.0	733	6	US-10-449-902-35674	Sequence 35674, A
38	41	68.3	306	7	US-11-330-403-1591	Sequence 1591, Ap
39	41	68.3	308	7	US-11-330-403-4913	Sequence 4913, Ap
40	40	66.7	311	7	US-11-330-403-2191	Sequence 2191, Ap
41	40	66.7	349	7	US-11-330-403-11569	Sequence 11569, A
42	40	66.7	463	7	US-11-330-403-10646	Sequence 10646, A
43	40	66.7	463	7	US-11-330-403-18424	Sequence 18424, A
44	40	66.7	878	6	US-10-449-902-41180	Sequence 41180, A
45	39	65.0	469	7	US-11-295-006-15	Sequence 15, Appl
46	38.5	64.2	444	7	US-11-174-307B-3704	Sequence 3704, Ap
47	38	63.3	288	7	US-11-330-403-18539	Sequence 18539, A
48	38	63.3	369	7	US-11-330-403-2219	Sequence 2219, Ap
49	38	63.3	526	7	US-11-174-307B-4392	Sequence 4392, Ap
50	37	61.7	17	6	US-10-522-086-13	Sequence 13, Appl
51	37	61.7	121	6	US-10-522-086-2	Sequence 2, Appli
52	37	61.7	170	6	US-10-449-902-48648	Sequence 48648, A
53	37	61.7	209	6	US-10-449-902-53763	Sequence 53763, A
54	37	61.7	247	7	US-11-270-894-1	Sequence 1, Appli
55	37	61.7	314	7	US-11-330-403-5311	Sequence 5311, Ap
56	37	61.7	328	7	US-11-330-403-18228	Sequence 18228, A
57	37	61.7	393	6	US-10-449-902-35268	Sequence 35268, A
58	37	61.7	415	6	US-10-449-902-53074	Sequence 53074, A
59	37	61.7	442	7	US-11-174-307B-2986	Sequence 2986, Ap

This page gives you Search Results detail for the Application 10661366 and Search Result us-10-661366-1. The results are sorted by relevance. You can click on the start

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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : PIR_80:*
 1: pir1:*
 2: pir2:*
 3: pir3:*
 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	57	95.0	104	2	S26466	Ig heavy chain V r
2	57	95.0	117	1	HVMSA1	Ig heavy chain pre
3	49	81.7	115	2	A54378	Ig heavy chain V r
4	48	80.0	67	2	H28833	Ig kappa chain V r
5	48	80.0	106	2	PH1002	Ig heavy chain V r
6	48	80.0	107	2	PH0999	Ig heavy chain V r
7	48	80.0	109	2	PH1001	Ig heavy chain V r
8	48	80.0	109	2	PH0997	Ig heavy chain V r
9	48	80.0	111	2	PH0998	Ig heavy chain V r
10	48	80.0	115	2	PL0238	Ig heavy chain V r
11	48	80.0	246	2	S38950	Ig gamma chain - m
12	48	80.0	446	2	S40295	Ig gamma-2a chain
13	47	78.3	112	2	PH0979	Ig heavy chain V r
14	44	73.3	351	2	AC2289	hypothetical prote
15	43	71.7	119	2	E30562	Ig heavy chain V r
16	43	71.7	292	2	AH1836	malonyl coenzyme A
17	43	71.7	293	2	S75355	probable [acyl-car
18	43	71.7	1728	2	T17466	rifamycin polyketi
19	43	71.7	4735	2	T17463	rifamycin polyketi
20	43	71.7	5069	2	T17464	rifamycin polyketi
21	42	70.0	364	2	A30521	myeloid cell surfa
22	42	70.0	469	2	S37483	Ig gamma-2a chain
23	42	70.0	642	2	G90551	lipoprotein [impor
24	40	66.7	91	2	PL0242	Ig heavy chain V r
25	40	66.7	107	2	PL0240	Ig heavy chain V r
26	40	66.7	107	2	PL0243	Ig heavy chain V r
27	40	66.7	107	2	PL0241	Ig heavy chain V r
28	40	66.7	120	2	F28195	Ig heavy chain V r
29	40	66.7	120	2	G28195	Ig heavy chain V r
30	40	66.7	138	2	S21810	Ig heavy chain V r
31	40	66.7	352	2	AI2297	histidinol-phospha
32	40	66.7	681	2	JX0338	rabphilin-3A - mou
33	40	66.7	684	2	I58166	rabphilin-3A - rat
34	40	66.7	1763	2	T17465	rifamycin polyketi
35	40	66.7	3413	2	T17467	rifamycin polyketi

SCORE Search Results Details for Application 10661366 and Search Result us-10-661-366-7.rup.

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OM protein - protein search, using sw model

Run on: August 9, 2006, 07:46:18 ; Search time 30.2389 Seconds
(without alignments)
305.902 Million cell updates/sec

Title: US-10-661-366-7
Perfect score: 60
Sequence: 1 WIFPGDGSTK 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	57	95.0	117	1 HV52_MOUSE	P06327 mus musculu
2	54	90.0	481	2 Q91WT1_MOUSE	Q91wt1 mus musculu
3	52	86.7	147	2 Q925S3_MOUSE	Q925s3 mus musculu
4	49	81.7	458	2 Q5BJZ2_RAT	Q5bjz2 rattus norv

5	47	78.3	298	2	Q31D44_PROM9	Q31d44	prochloroco
6	47	78.3	298	2	Q3AH13_SYNSC	Q3ah13	synechococc
7	47	78.3	298	2	Q3B050_SYNS9	Q3b050	synechococc
8	47	78.3	298	2	Q46HN7_PROMT	Q46hn7	prochloroco
9	47	78.3	298	2	Q7U426_SYNPX	Q7u426	synechococc
10	47	78.3	298	2	Q7V3D9_PROMP	Q7v3d9	prochloroco
11	47	78.3	298	2	Q7V4F5_PROMM	Q7v4f5	prochloroco
12	47	78.3	322	2	Q4BXV4_CROWT	Q4bxv4	crocospaer
13	45	75.0	1092	2	Q3JTK6_BURP1	Q3jtk6	burkholderi
14	45	75.0	1101	2	Q6JIL2_9CAUD	Q6jil2	bacteriopha
15	45	75.0	1101	2	Q8W6T0_9CAUD	Q8w6t0	bacteriopha
16	45	75.0	1101	2	Q2T6E0_BURTH	Q2t6e0	burkholderi
17	44	73.3	118	2	Q4IG30_GIBZE	Q4ig30	gibberella
18	44	73.3	295	2	Q7NIN8_GLOVI	Q7nin8	gloeobacter
19	44	73.3	335	2	Q33JU3_METHU	Q33ju3	methanospir
20	44	73.3	347	2	Q3MC37_ANAVT	Q3mc37	anabaena va
21	44	73.3	351	2	Q8YQG5_ANASP	Q8yqg5	anabaena sp
22	44	73.3	480	2	Q8K0Z4_MOUSE	Q8k0z4	mus musculu
23	43	71.7	290	2	Q4C5L8_CROWT	Q4c5l8	crocospaer
24	43	71.7	292	2	Q3M9J3_ANAVT	Q3m9j3	anabaena va
25	43	71.7	292	2	Q8Z061_ANASP	Q8z061	anabaena sp
26	43	71.7	293	1	FABD_SYNY3	P73242	synechocyst
27	43	71.7	293	2	Q31N83_SYNP7	Q31n83	synechococc
28	43	71.7	293	2	Q5N5X6_SYNP6	Q5n5x6	synechococc
29	43	71.7	298	2	Q7VE54_PROMA	Q7ve54	prochloroco
30	43	71.7	309	2	Q3CCK1_ALTAT	Q3cxk1	pseudoalter
31	43	71.7	311	2	Q4ZZA4_PSEU2	Q4zza4	pseudomonas
32	43	71.7	318	2	Q3DVH3_CHIAU	Q3dvh3	chloroflexu
33	43	71.7	695	2	Q7SA97_NEUCR	Q7sa97	neurospora
34	43	71.7	1100	2	Q3HQU5_9CAUD	Q3hqu5	burkholderi
35	43	71.7	1191	2	Q9RHV0_STRRO	Q9rhv0	streptomyce
36	43	71.7	1728	2	O54591_AMYMD	O54591	amycolatops
37	43	71.7	3295	2	Q83X71_STRRO	Q83x71	streptomyce
38	43	71.7	3651	2	Q83X69_STRRO	Q83x69	streptomyce
39	43	71.7	4735	2	O54666_AMYMD	O54666	amycolatops
40	43	71.7	5060	2	O52545_AMYMD	O52545	amycolatops
41	43	71.7	5069	2	O52789_AMYMD	O52789	amycolatops
42	42	70.0	298	2	Q8DMS0_SYNEL	Q8dms0	synechococc
43	42	70.0	364	1	CD33_HUMAN	P20138	homo sapien
44	42	70.0	364	2	Q546G0_HUMAN	Q546g0	homo sapien
45	42	70.0	400	2	Q3SUE5_NITWN	Q3sue5	nitrobacter
46	42	70.0	438	2	Q7V5W9_PROMM	Q7v5w9	prochloroco
47	42	70.0	519	2	Q8S7D9_ORYSA	Q8s7d9	oryza sativ
48	42	70.0	542	2	Q336R0_ORYSA	Q336r0	oryza sativ
49	42	70.0	601	2	Q8JH43_BRARE	Q8jh43	brachydanio
50	42	70.0	601	2	Q6P4V3_BRARE	Q6p4v3	brachydanio
51	42	70.0	614	2	Q84SM9_ORYSA	Q84sm9	oryza sativ
52	42	70.0	642	2	Q98QP2_MYCPU	Q98qp2	mycoplasma
53	42	70.0	733	2	Q658I3_ORYSA	Q658i3	oryza sativ
54	42	70.0	2193	2	Q2SGN0_9GAMM	Q2sgn0	hahella che
55	42	70.0	2941	2	Q7UEZ5_RHOBA	Q7uez5	rhodopirell
56	41	68.3	288	2	Q2JJA3_9CYAN	Q2jja3	cyanobacter
57	41	68.3	289	2	Q2JS91_9CYAN	Q2js91	cyanobacter
58	41	68.3	306	2	Q41D37_9BACI	Q41d37	exiguobacte
59	41	68.3	308	2	Q6FBG4_ACIAAD	Q6fbg4	acinetobact
60	41	68.3	969	2	Q8BPR2_MOUSE	Q8bpr2	mus musculu
61	41	68.3	1258	2	Q70IV4_MOUSE	Q70iv4	mus musculu
62	41	68.3	1259	2	Q3UPZ4_MOUSE	Q3upz4	mus musculu
63	41	68.3	1292	2	Q6A081_MOUSE	Q6a081	mus musculu
64	41	68.3	1560	2	Q70IV5_MOUSE	Q70iv5	mus musculu
65	40	66.7	88	2	Q4CEP8_CLOTM	Q4cep8	clostridium

http://es/ScoreAccessWeb/GetItem.action?AppId=10661366&seqId=580918&ItemName=us... 8/11/06

Result No.	Score	% Query Match	Length	DB	ID	Description
1	52	55.9	15	8	ADR45758	Adr45758 Peptide d
2	49	52.7	11	4	AAG62989	Aag62989 Complemen
3	49	52.7	11	4	AAU02698	Aau02698 CDR regio
4	48.5	52.2	13	2	AAR50321	Aar50321 MAb NFS2
5	48	51.6	13	9	ADW47117	Adw47117 Anti-CD20
6	48	51.6	14	8	ADL27494	Adl27494 CDR from
7	48	51.6	15	9	ADV14586	Adv14586 CDR3 pept
8	48	51.6	15	9	ADX58332	Adx58332 Amino aci
9	45	48.4	11	7	ABR82936	Abr82936 Anti-huma
10	45	48.4	13	2	AAV41198	Aay41198 CDR pepti
11	45	48.4	13	9	ADW47118	Adw47118 Anti-CD20
12	45	48.4	14	9	AED12589	Aed12589 Anti-Nogo
13	44	47.3	12	2	AAV41199	Aay41199 CDR pepti
14	44	47.3	14	2	AAV41197	Aay41197 CDR pepti
15	44	47.3	15	5	ABP46723	Abp46723 Human BLY
16	44	47.3	15	7	ADG97550	Adg97550 scFV VHCD
17	44	47.3	15	9	AED79603	Aed79603 Human B L
18	43.5	46.8	12	10	AEF77053	Aef77053 Antibody
19	43.5	46.8	12	10	AEF76349	Aef76349 Prostate
20	43	46.2	10	9	ADZ45492	Adz45492 Murine fa
21	43	46.2	12	9	AEA45964	Aea45964 Apolipop
22	43	46.2	13	10	AEG03156	Aeg03156 CD200-spe
23	43	46.2	14	2	AAW70907	Aaw70907 CDR3 of t
24	43	46.2	14	2	AAW70931	Aaw70931 CDR3 of t
25	43	46.2	14	5	AAU99859	Aau99859 Mouse HeF
26	43	46.2	14	7	AAO29933	Aao29933 Mouse ant
27	43	46.2	14	8	ADJ87926	Adj87926 Mouse HeF
28	42	45.2	13	10	AEG03147	Aeg03147 CD200-spe
29	42	45.2	15	2	AAV41187	Aay41187 CDR pepti
30	42	45.2	15	10	AEE73502	Aee73502 Anti-Wnt2
31	41.5	44.6	14	8	ADM78134	Adm78134 Human SJB
32	41	44.1	12	4	AAG63990	Aag63990 Complemen
33	41	44.1	12	6	ABU87176	Abu87176 Carbohydr
34	41	44.1	13	8	ADM46727	Adm46727 Variant a
35	41	44.1	13	8	ADQ95027	Adq95027 Synthetic
36	41	44.1	14	4	AAB35580	Aab35580 Meningoco
37	41	44.1	14	8	ADM10972	Adm10972 GPIIbIIIa
38	41	44.1	14	9	AEA14637	Aea14637 VEGF rela
39	40.5	43.5	13	2	AAW70925	Aaw70925 CDR3 of t
40	40.5	43.5	13	9	ADZ45412	Adz45412 Murine fa
41	40.5	43.5	15	9	ADY75243	Ady75243 Clone D12
42	40	43.0	13	7	ADD94157	Add94157 Mouse HUI
43	40	43.0	13	7	ADD94214	Add94214 Mouse HUI
44	40	43.0	13	7	ADD94212	Add94212 Mouse HUI
45	40	43.0	13	7	ADD94215	Add94215 Mouse HUI
46	40	43.0	13	7	ADD94213	Add94213 Mouse HUI
47	40	43.0	13	7	ADD94211	Add94211 Mouse HUI
48	40	43.0	13	10	AEG03146	Aeg03146 CD200-spe
49	40	43.0	14	9	AEA14624	Aea14624 VEGF rela
50	39.5	42.5	12	8	ADO43577	Ado43577 Complemen
51	39.5	42.5	14	9	AEA14238	Aea14238 VEGF rela
52	39	41.9	7	9	ADW10780	Adw10780 Heavy cha
53	39	41.9	8	10	AEF76351	Aef76351 Prostate
54	39	41.9	11	4	AAB62863	Aab62863 Anti-SAF-
55	39	41.9	11	7	ADD94172	Add94172 Mouse HUI
56	39	41.9	13	8	ADS88066	Ads88066 Human CD2
57	39	41.9	13	8	ADS88072	Ads88072 Human CD2

SCORE Search Results Details for Application 10661366 and Search Result us-10-661-366-8.closed.ra

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OM protein - protein search, using sw model

Run on: August 9, 2006, 07:02:53 ; Search time 39.3443 Seconds
(without alignments)
35.596 Million cell updates/sec

Title: US-10-661-366-8
Perfect score: 93
Sequence: 1 SAYYRYDGSYYAMDY 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 249102

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Database : Issued_Patents_AA:*
1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB ID	Description
1	48.5	52.2	13	5	PCT-US93-08435-20 Sequence 20, Appl
2	48	51.6	14	2	US-10-226-795-35 Sequence 35, Appl

3	41	44.1	15	2	US-09-025-769B-179	Sequence 179, App
4	41	44.1	15	2	US-09-490-070A-179	Sequence 179, App
5	41	44.1	15	2	US-09-490-153-179	Sequence 179, App
6	41	44.1	15	2	US-09-490-324-179	Sequence 179, App
7	39	41.9	12	2	US-09-091-071-8	Sequence 8, Appli
8	38	40.9	12	1	US-08-360-125-24	Sequence 24, Appl
9	38	40.9	12	1	US-08-450-578-24	Sequence 24, Appl
10	38	40.9	12	1	US-09-017-628-24	Sequence 24, Appl
11	38	40.9	12	1	US-09-014-880-24	Sequence 24, Appl
12	38	40.9	12	2	US-08-450-363-24	Sequence 24, Appl
13	38	40.9	12	2	US-09-467-903-24	Sequence 24, Appl
14	38	40.9	13	2	US-09-914-695-32	Sequence 32, Appl
15	36	38.7	10	2	US-08-993-165-11	Sequence 11, Appl
16	36	38.7	10	2	US-09-540-448-11	Sequence 11, Appl
17	36	38.7	10	2	US-09-243-640-9	Sequence 9, Appli
18	36	38.7	10	2	US-08-929-847-11	Sequence 11, Appl
19	36	38.7	10	2	US-09-813-484-11	Sequence 11, Appl
20	36	38.7	10	2	US-10-046-801-11	Sequence 11, Appl
21	36	38.7	14	1	US-08-737-085A-1	Sequence 1, Appli
22	36	38.7	14	2	US-08-467-580-144	Sequence 144, App
23	36	38.7	14	2	US-09-246-258-1	Sequence 1, Appli
24	36	38.7	14	2	US-09-532-106-1	Sequence 1, Appli
25	36	38.7	14	2	US-09-839-666-1	Sequence 1, Appli
26	36	38.7	14	2	US-10-372-735-43	Sequence 43, Appl
27	36	38.7	14	5	PCT-US95-08516-144	Sequence 144, App
28	36	38.7	15	2	US-09-638-202A-11	Sequence 11, Appl
29	36	38.7	15	2	US-09-096-749A-11	Sequence 11, Appl
30	36	38.7	15	2	US-09-637-614-11	Sequence 11, Appl
31	35	37.6	14	2	US-08-914-372C-16	Sequence 16, Appl
32	34.5	37.1	12	1	US-07-946-421-6	Sequence 6, Appli
33	34.5	37.1	14	2	US-09-424-712-30	Sequence 30, Appl
34	34	36.6	13	2	US-08-908-469-81	Sequence 81, Appl
35	34	36.6	14	5	PCT-US94-14106-48	Sequence 48, Appl
36	34	36.6	15	2	US-09-347-504-45	Sequence 45, Appl
37	34	36.6	15	2	US-10-161-499-45	Sequence 45, Appl
38	33.5	36.0	10	2	US-09-254-180C-3	Sequence 3, Appli
39	33	35.5	10	1	US-08-480-434-28	Sequence 28, Appl
40	33	35.5	10	1	US-08-480-434-35	Sequence 35, Appl
41	33	35.5	10	1	US-08-053-451B-28	Sequence 28, Appl
42	33	35.5	10	1	US-08-053-451B-35	Sequence 35, Appl
43	33	35.5	12	1	US-08-360-125-17	Sequence 17, Appl
44	33	35.5	12	1	US-08-450-578-17	Sequence 17, Appl
45	33	35.5	12	1	US-09-017-628-17	Sequence 17, Appl
46	33	35.5	12	1	US-09-014-880-17	Sequence 17, Appl
47	33	35.5	12	2	US-08-450-363-17	Sequence 17, Appl
48	33	35.5	12	2	US-09-467-903-17	Sequence 17, Appl
49	33	35.5	13	1	US-08-737-085A-2	Sequence 2, Appli
50	33	35.5	13	2	US-09-246-258-2	Sequence 2, Appli
51	33	35.5	13	2	US-09-532-106-2	Sequence 2, Appli
52	33	35.5	13	2	US-09-839-666-2	Sequence 2, Appli
53	33	35.5	13	2	US-08-908-469-71	Sequence 71, Appl
54	33	35.5	13	2	US-10-372-735-44	Sequence 44, Appl
55	32	34.4	5	2	US-09-149-997B-1	Sequence 1, Appli
56	32	34.4	6	2	US-09-149-997B-2	Sequence 2, Appli
57	32	34.4	11	2	US-08-525-539A-42	Sequence 42, Appl
58	32	34.4	14	2	US-08-914-372C-19	Sequence 19, Appl
59	32	34.4	15	2	US-08-992-877-53	Sequence 53, Appl
60	32	34.4	15	2	US-09-517-866-6	Sequence 6, Appli
61	32	34.4	15	3	US-10-279-991A-6	Sequence 6, Appli
62	31	33.3	8	2	US-09-453-718B-17	Sequence 17, Appl
63	31	33.3	9	2	US-09-517-866-8	Sequence 8, Appli

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OM protein - protein search, using sw model

Run on: August 9, 2006, 07:35:38 ; Search time 127.213 Seconds
(without alignments)
58.260 Million cell updates/sec

Title: US-10-661-366-8
Perfect score: 93
Sequence: 1 SAYYRYDGSYYAMDY 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 395127

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Database : Published_Applications_AA_Main:*
1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB ID	Description
1	52	55.9	15	4	US-10-772-089-3
2	48	51.6	14	4	US-10-226-795-35
3	48	51.6	15	5	US-10-903-858-21

4	45	48.4	11	4	US-10-372-719-19	Sequence 19, Appl
5	45	48.4	11	5	US-10-505-747-19	Sequence 19, Appl
6	45	48.4	13	3	US-09-252-150-73	Sequence 73, Appl
7	45	48.4	13	5	US-10-646-381-73	Sequence 73, Appl
8	45	48.4	13	6	US-11-128-440-73	Sequence 73, Appl
9	44	47.3	12	3	US-09-252-150-74	Sequence 74, Appl
10	44	47.3	12	5	US-10-646-381-74	Sequence 74, Appl
11	44	47.3	12	6	US-11-128-440-74	Sequence 74, Appl
12	44	47.3	14	3	US-09-252-150-72	Sequence 72, Appl
13	44	47.3	14	5	US-10-646-381-72	Sequence 72, Appl
14	44	47.3	14	6	US-11-128-440-72	Sequence 72, Appl
15	44	47.3	15	3	US-09-880-748-2734	Sequence 2734, Ap
16	44	47.3	15	4	US-10-293-418-2734	Sequence 2734, Ap
17	44	47.3	15	6	US-11-054-515-2734	Sequence 2734, Ap
18	44	47.3	15	6	US-11-266-444-2734	Sequence 2734, Ap
19	43	46.2	13	5	US-10-996-316-199	Sequence 199, App
20	43	46.2	13	6	US-11-171-567-199	Sequence 199, App
21	43	46.2	14	4	US-10-447-257-24	Sequence 24, Appl
22	43	46.2	14	5	US-10-496-628-24	Sequence 24, Appl
23	42	45.2	13	5	US-10-996-316-190	Sequence 190, App
24	42	45.2	13	6	US-11-171-567-190	Sequence 190, App
25	42	45.2	15	3	US-09-252-150-62	Sequence 62, Appl
26	42	45.2	15	5	US-10-646-381-62	Sequence 62, Appl
27	42	45.2	15	6	US-11-128-440-62	Sequence 62, Appl
28	42	45.2	15	6	US-11-131-425A-91	Sequence 91, Appl
29	41	44.1	12	3	US-09-894-594-67	Sequence 67, Appl
30	41	44.1	12	4	US-10-232-187-7	Sequence 7, Appli
31	41	44.1	13	5	US-10-759-731A-24	Sequence 24, Appl
32	41	44.1	13	5	US-10-939-309-31	Sequence 31, Appl
33	41	44.1	15	5	US-10-834-397-179	Sequence 179, App
34	40	43.0	13	3	US-09-995-529-42	Sequence 42, Appl
35	40	43.0	13	3	US-09-995-529-96	Sequence 96, Appl
36	40	43.0	13	3	US-09-995-529-97	Sequence 97, Appl
37	40	43.0	13	3	US-09-995-529-98	Sequence 98, Appl
38	40	43.0	13	3	US-09-995-529-99	Sequence 99, Appl
39	40	43.0	13	3	US-09-995-529-100	Sequence 100, App
40	40	43.0	13	3	US-09-995-529-42	Sequence 42, Appl
41	40	43.0	13	3	US-09-995-529-96	Sequence 96, Appl
42	40	43.0	13	3	US-09-995-529-97	Sequence 97, Appl
43	40	43.0	13	3	US-09-995-529-98	Sequence 98, Appl
44	40	43.0	13	3	US-09-995-529-99	Sequence 99, Appl
45	40	43.0	13	3	US-09-995-529-100	Sequence 100, App
46	40	43.0	13	5	US-10-996-316-189	Sequence 189, App
47	40	43.0	13	6	US-11-171-567-189	Sequence 189, App
48	39	41.9	11	3	US-09-995-529-57	Sequence 57, Appl
49	39	41.9	11	3	US-09-995-529-57	Sequence 57, Appl
50	39	41.9	13	4	US-10-687-799-15	Sequence 15, Appl
51	39	41.9	13	4	US-10-687-799-21	Sequence 21, Appl
52	38.5	41.4	11	6	US-11-009-939-5	Sequence 5, Appli
53	38	40.9	12	5	US-10-996-316-191	Sequence 191, App
54	38	40.9	12	5	US-10-507-662-53	Sequence 53, Appl
55	38	40.9	12	6	US-11-171-567-191	Sequence 191, App
56	38	40.9	13	4	US-10-762-629-32	Sequence 32, Appl
57	38	40.9	13	5	US-10-783-311-285	Sequence 285, App
58	38	40.9	13	5	US-10-783-311-317	Sequence 317, App
59	38	40.9	14	3	US-09-252-150-63	Sequence 63, Appl
60	38	40.9	14	4	US-10-697-399-43	Sequence 43, Appl
61	38	40.9	14	4	US-10-697-399-45	Sequence 45, Appl
62	38	40.9	14	5	US-10-646-381-63	Sequence 63, Appl
63	38	40.9	14	6	US-11-128-440-63	Sequence 63, Appl
64	38	40.9	15	3	US-09-880-748-2983	Sequence 2983, Ap

SCORE Search Results Details for Application 10661366 and Search Result us-10-661-366-8.closed.rapbn.

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Page	List	Overview	FAQ	Suggestions

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OM protein - protein search, using sw model

Run on: August 9, 2006, 07:36:48 ; Search time 20.1967 Seconds
(without alignments)
53.325 Million cell updates/sec

Title: US-10-661-366-8
Perfect score: 93
Sequence: 1 SAYRYDGSYYYAMDY 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 239914 seqs, 67312017 residues

Total number of hits satisfying chosen parameters: 27373

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Database : Published_Applications_AA_New:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	% Query
--------	------------

No.	Score	Match	Length	DB	ID	Description
1	38.5	41.4	11	7	US-11-301-373-5	Sequence 5, Appli
2	36	38.7	11	6	US-10-484-105-5	Sequence 5, Appli
3	36	38.7	14	7	US-11-121-282-43	Sequence 43, Appl
4	33	35.5	10	6	US-10-537-642-74	Sequence 74, Appl
5	33	35.5	11	6	US-10-542-508-9	Sequence 9, Appli
6	33	35.5	11	7	US-11-196-917A-152	Sequence 152, App
7	33	35.5	13	7	US-11-121-282-44	Sequence 44, Appl
8	31.5	33.9	13	7	US-11-094-132-45	Sequence 45, Appl
9	31	33.3	9	7	US-11-242-617-38	Sequence 38, Appl
10	31	33.3	11	6	US-10-542-508-6	Sequence 6, Appli
11	31	33.3	11	6	US-10-542-508-42	Sequence 42, Appl
12	31	33.3	11	7	US-11-242-617-110	Sequence 110, App
13	30	32.3	11	6	US-10-542-508-26	Sequence 26, Appl
14	30	32.3	11	6	US-10-542-508-35	Sequence 35, Appl
15	30	32.3	11	6	US-10-542-682-43	Sequence 43, Appl
16	29.5	31.7	15	7	US-11-196-917A-171	Sequence 171, App
17	29	31.2	10	6	US-10-542-682-36	Sequence 36, Appl
18	29	31.2	11	7	US-11-196-917A-113	Sequence 113, App
19	29	31.2	11	7	US-11-196-917A-154	Sequence 154, App
20	29	31.2	14	6	US-10-991-309B-73	Sequence 73, Appl
21	28	30.1	11	7	US-11-196-917A-6	Sequence 6, Appli
22	28	30.1	11	7	US-11-196-917A-7	Sequence 7, Appli
23	28	30.1	11	7	US-11-196-917A-8	Sequence 8, Appli
24	28	30.1	11	7	US-11-196-917A-114	Sequence 114, App
25	28	30.1	11	7	US-11-196-917A-123	Sequence 123, App
26	28	30.1	11	7	US-11-196-917A-124	Sequence 124, App
27	28	30.1	11	7	US-11-196-917A-125	Sequence 125, App
28	28	30.1	11	7	US-11-196-917A-142	Sequence 142, App
29	28	30.1	11	7	US-11-196-917A-143	Sequence 143, App
30	28	30.1	11	7	US-11-196-917A-153	Sequence 153, App
31	28	30.1	15	7	US-11-196-917A-172	Sequence 172, App
32	28	30.1	15	7	US-11-196-917A-173	Sequence 173, App
33	27.5	29.6	11	7	US-11-196-917A-131	Sequence 131, App
34	27.5	29.6	11	7	US-11-301-373-35	Sequence 35, Appl
35	27	29.0	9	7	US-11-263-230-1495	Sequence 1495, Ap
36	27	29.0	11	7	US-11-196-917A-122	Sequence 122, App
37	27	29.0	11	7	US-11-196-917A-136	Sequence 136, App
38	27	29.0	11	7	US-11-196-917A-163	Sequence 163, App
39	27	29.0	12	6	US-10-991-309B-46	Sequence 46, Appl
40	27	29.0	13	7	US-11-254-182-62	Sequence 62, Appl
41	27	29.0	13	7	US-11-106-762-16	Sequence 16, Appl
42	27	29.0	13	7	US-11-313-356-19	Sequence 19, Appl
43	27	29.0	13	7	US-11-291-698A-52	Sequence 52, Appl
44	27	29.0	14	6	US-10-499-266-17	Sequence 17, Appl
45	27	29.0	15	6	US-10-984-473-27	Sequence 27, Appl
46	27	29.0	15	7	US-11-196-917A-178	Sequence 178, App
47	26.5	28.5	11	7	US-11-196-917A-118	Sequence 118, App
48	26.5	28.5	11	7	US-11-390-775-66	Sequence 66, Appl
49	26.5	28.5	13	7	US-11-061-841-277	Sequence 277, App
50	26	28.0	7	6	US-10-539-402-103	Sequence 103, App
51	26	28.0	7	6	US-10-522-086-29	Sequence 29, Appl
52	26	28.0	9	6	US-10-537-642-75	Sequence 75, Appl
53	26	28.0	11	6	US-10-540-431-2	Sequence 2, Appli
54	26	28.0	11	6	US-10-542-508-11	Sequence 11, Appl
55	26	28.0	11	6	US-10-542-508-14	Sequence 14, Appl
56	26	28.0	11	6	US-10-542-508-24	Sequence 24, Appl
57	26	28.0	11	6	US-10-542-508-30	Sequence 30, Appl
58	26	28.0	11	6	US-10-542-508-32	Sequence 32, Appl
59	26	28.0	11	6	US-10-542-508-36	Sequence 36, Appl

SCORE Search

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OM protein - protein search, using sw model

Run on: August 9, 2006, 06:51:47 ; Search time 22.0328 Seconds
 (without alignments)
 69.872 Million cell updates/sec

Title: US-10-661-366-8
 Perfect score: 93
 Sequence: 1 SAYYRYDGSYYYAMDY 16

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 2523

Minimum DB seq length: 0
 Maximum DB seq length: 15

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 500 summaries

Database : PIR_80:*
 1: pir1:*
 2: pir2:*
 3: pir3:*
 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%					Description
	No.	Score	Query Match	Length	ID	
1	50	53.8	14	2	PH1608	Ig H chain V-D-J r
2	47.5	51.1	15	2	PH1610	Ig H chain V-D-J r
3	45	48.4	12	2	PH1606	Ig H chain V-D-J r
4	45	48.4	14	2	PH1597	Ig H chain V-D-J r
5	43	46.2	13	2	PH1596	Ig H chain V-D-J r
6	43	46.2	14	2	PH1601	Ig H chain V-D-J r
7	38.5	41.4	15	2	PH1582	Ig H chain V-D-J r
8	38	40.9	13	2	PH1593	Ig H chain V-D-J r

9	36	38.7	11	2	PH1632	Ig H chain V-D-J r
10	36	38.7	14	2	PH1615	Ig H chain V-D-J r
11	33	35.5	14	2	PT0252	Ig heavy chain CRD
12	32.5	34.9	14	2	PH1586	Ig H chain V-D-J r
13	30.5	32.8	14	2	PH1623	Ig H chain V-D-J r
14	29.5	31.7	15	2	PH1631	Ig H chain V-D-J r
15	29	31.2	12	2	PH1587	Ig H chain V-D-J r
16	29	31.2	13	2	PH1595	Ig H chain V-D-J r
17	29	31.2	14	2	PH1614	Ig H chain V-D-J r
18	29	31.2	14	2	PH1617	Ig H chain V-D-J r
19	28.5	30.6	14	2	PT0232	Ig heavy chain CRD
20	27.5	29.6	9	2	S36850	Ig heavy chain V r
21	27	29.0	12	2	S25056	Ig heavy chain - m
22	27	29.0	12	2	PH1324	Ig heavy chain DJ
23	27	29.0	12	2	PH1611	Ig H chain V-D-J r
24	25.5	27.4	12	2	PH1605	Ig H chain V-D-J r
25	25.5	27.4	14	2	PH1598	Ig H chain V-D-J r
26	25	26.9	8	2	S68325	blood cell protein
27	25	26.9	13	2	S47358	T-cell antigen rec
28	23	24.7	9	2	S70334	endosperm protein,
29	23	24.7	9	2	D57444	neuropeptide Grb-A
30	23	24.7	14	2	PT0254	Ig heavy chain CRD
31	23	24.7	15	2	PH1319	Ig heavy chain DJ
32	22.5	24.2	14	1	NYPG14	hypothalamic tetra
33	22	23.7	7	2	PC2132	FMRFamide-related
34	22	23.7	9	2	PT0285	Ig heavy chain CRD
35	22	23.7	10	2	PT0291	Ig heavy chain CRD
36	22	23.7	10	2	PH1592	Ig H chain V-D-J r
37	22	23.7	10	2	F33932	Ig mu chain J regi
38	22	23.7	11	2	S68392	H+-transporting tw
39	22	23.7	11	2	PH1600	Ig H chain V-D-J r
40	22	23.7	12	2	PH1581	Ig H chain V-D-J r
41	22	23.7	13	2	PH1585	Ig H chain V-D-J r
42	22	23.7	14	2	S39931	S-allele-associate
43	22	23.7	15	2	PH1613	Ig H chain V-D-J r
44	22	23.7	15	2	PT0091	H+-transporting tw
45	21.5	23.1	15	2	PH1366	Ig heavy chain DJ
46	21	22.6	9	2	S70332	endosperm protein,
47	21	22.6	10	2	PT0243	Ig heavy chain CRD
48	21	22.6	10	2	PC4442	cytochrome c553 -
49	21	22.6	11	2	PT0302	Ig heavy chain CRD
50	21	22.6	12	2	S47391	T-cell antigen rec
51	21	22.6	12	2	S47395	T-cell antigen rec
52	21	22.6	13	2	S47372	T-cell antigen rec
53	21	22.6	13	2	S47384	T-cell antigen rec
54	21	22.6	14	2	S39930	S-allele-associate
55	21	22.6	14	2	E33098	214K exoantigen (v
56	21	22.6	14	2	PT0294	Ig heavy chain CRD
57	21	22.6	15	2	PH1365	Ig heavy chain DJ
58	21	22.6	15	2	S47387	T-cell antigen rec
59	20	21.5	8	2	PT0030	inulinase (EC 3.2.
60	20	21.5	9	2	S10784	enamelin i - bovin
61	20	21.5	11	2	B41946	T-cell receptor ga
62	20	21.5	12	2	PN0170	alcohol dehydrogen
63	20	21.5	13	2	S47371	T-cell antigen rec
64	20	21.5	14	2	A58963	alpha-conotoxin Cn
65	20	21.5	15	2	A48372	benzoyl-CoA ligase
66	20	21.5	15	2	A56970	GLYMA1 - soybean (
67	20	21.5	15	2	S65429	pyrogallol hydroxy
68	19	20.4	7	4	I56695	hypothetical L2 pr
69	19	20.4	9	2	A37027	macrophage chemota

SCORE Search Results Details for Application 10661366 and Search Result us-10-661-366-8.closed.rup.

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OM protein - protein search, using sw model

Run on: August 9, 2006, 06:40:52 ; Search time 178.361 Seconds
(without alignments)
82.979 Million cell updates/sec

Title: US-10-661-366-8
Perfect score: 93
Sequence: 1 SAYYRYDGSYYYAMDY 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 8966

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Database : UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	37	39.8	10	2 Q53VQ3_MOUSE	Q53vq3 mus musculu
2	36	38.7	11	2 Q53VR4_MOUSE	Q53vr4 mus musculu
3	33	35.5	10	2 Q53VQ7_MOUSE	Q53vq7 mus musculu
4	31	33.3	15	2 P93516_ARATH	P93516 arabidopsis

5	30	32.3	11	2	Q53VQ6_MOUSE	Q53vq6	mus musculus
6	28	30.1	10	2	Q53VR1_MOUSE	Q53vr1	mus musculus
7	28	30.1	13	2	Q7S2J9_NEUCR	Q7s2j9	neurospora
8	26	28.0	11	2	Q90WA2_CHICK	Q90wa2	gallus gall
9	26	28.0	15	1	UC14_MAIZE	P80620	zea mays (m
10	26	28.0	15	2	P93515_ARATH	P93515	arabidopsis
11	25	26.9	8	2	Q7M3L7_9ASCI	Q7m3l7	ascidia cer
12	25	26.9	11	2	Q9UC46_HUMAN	Q9uc46	homo sapien
13	24	25.8	10	1	UH05_RAT	P56573	rattus norv
14	24	25.8	15	1	OLP_TOBAC	P80781	nicotiana t
15	23	24.7	9	2	Q7M3N6_GRYBI	Q7m3n6	gryllus bim
16	23	24.7	11	1	ASL1_BACSE	P83146	bacteroides
17	23	24.7	13	1	ADFB_TENMO	P83109	tenebrio mo
18	23	24.7	15	2	Q4X8J7_PLACH	Q4x8j7	plasmodium
19	22.5	24.2	14	1	HY14_PIG	P01155	sus scrofa
20	22	23.7	7	1	FAR3_HAECO	P81298	haemonchus
21	22	23.7	7	1	FAR3_PANRE	P41874	panagrellus
22	22	23.7	8	2	Q4X617_PLACH	Q4x617	plasmodium
23	22	23.7	10	2	O54217_STAEP	O54217	staphylococ
24	22	23.7	11	2	Q70Y64_9LAMI	Q70y64	plectranthu
25	22	23.7	11	2	Q53VR0_MOUSE	Q53vr0	mus musculus
26	22	23.7	12	1	CWP13_PHAVU	P80772	phaseolus v
27	22	23.7	12	2	Q7RFX5_PLAYO	Q7rfx5	plasmodium
28	22	23.7	13	1	TXMO1_CONMO	P84713	conus monil
29	22	23.7	13	2	Q7ZT28_MOTFL	Q7zt28	motacilla f
30	22	23.7	13	2	Q7ZT29_MOTCT	Q7zt29	motacilla c
31	22	23.7	13	2	Q7ZZI4_MOTFL	Q7zzi4	motacilla f
32	22	23.7	13	2	Q7ZZI5_MOTFL	Q7zzi5	motacilla f
33	22	23.7	13	2	Q7ZZI7_MOTFL	Q7zzi7	motacilla f
34	22	23.7	13	2	Q7ZZI8_MOTFL	Q7zzi8	motacilla f
35	22	23.7	13	2	Q7ZZJ0_MOTFL	Q7zzj0	motacilla f
36	22	23.7	13	2	Q7ZZJ1_MOTFL	Q7zzj1	motacilla f
37	22	23.7	13	2	Q7ZZJ3_MOTFL	Q7zzj3	motacilla f
38	22	23.7	13	2	Q7ZZJ4_MOTCT	Q7zzj4	motacilla c
39	22	23.7	13	2	Q7ZZJ5_MOTCI	Q7zzj5	motacilla c
40	22	23.7	13	2	Q7ZZJ6_9PASS	Q7zzj6	anthus prat
41	22	23.7	14	2	Q7M261_PYRPY	Q7m261	pyrus pyrif
42	22	23.7	15	1	UP01_METAN	P83440	metarhizium
43	22	23.7	15	2	Q71UI1_CANFA	Q71ui1	canis famil
44	22	23.7	15	2	Q33AF6_ORYSA	Q33af6	oryza sativ
45	21	22.6	10	2	Q7RSI4_PLAYO	Q7rsi4	plasmodium
46	21	22.6	10	2	Q7MOM6_DESDE	Q7m0m6	desulfovibr
47	21	22.6	11	1	CAE42_LITCI	P82092	litoria cit
48	21	22.6	12	2	Q4X448_PLACH	Q4x448	plasmodium
49	21	22.6	12	2	Q41856_MAIZE	Q41856	zea mays (m
50	21	22.6	13	2	Q50L81_9DIPT	Q50l81	drosophila
51	21	22.6	13	2	Q71A29_PIG	Q71a29	sus scrofa
52	21	22.6	14	1	GSTE1_PSEPU	P82996	pseudomonas
53	21	22.6	14	2	Q50L76_DROAN	Q50l76	drosophila
54	21	22.6	14	2	Q70Y91_9LAMI	Q70y91	platostoma
55	21	22.6	14	2	Q54394_STRLI	Q54394	streptomyce
56	21	22.6	15	2	Q6TAR1_HUMAN	Q6tar1	homo sapien
57	21	22.6	15	2	Q9UJ51_HUMAN	Q9uj51	homo sapien
58	21	22.6	15	2	Q2XT21_CHICK	Q2xt21	gallus gall
59	20.5	22.0	11	1	CAE41_LITCI	P82091	litoria cit
60	20	21.5	8	2	Q7M4U4_ASPFI	Q7m4u4	aspergillus
61	20	21.5	8	2	Q68LF1_9PASS	Q68lf1	myrmotherul
62	20	21.5	8	2	Q68LG3_9PASS	Q68lg3	sakesphorus
63	20	21.5	9	2	Q7M2M7_BOVIN	Q7m2m7	bos taurus
64	20	21.5	10	1	AMPN_HELAM	P81731	helicoverpa
65	20	21.5	11	2	Q7ZZI6_MOTFL	Q7zzi6	motacilla f

SCORE Search Results Details for Application 10661366 and Search Result us-10-661-366-8.rag.

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OM protein - protein search, using sw model

Run on: August 9, 2006, 07:45:18 ; Search time 40.4096 Seconds
(without alignments)
181.033 Million cell updates/sec

Title: US-10-661-366-8
Perfect score: 93
Sequence: 1 SAYYRYDGSYYYAMDY 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : A_Geneseq_8:*
1: geneseqp1980s:*
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4: geneseqp2001s:*
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6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	93	100.0	125	9	ADY75166	Ady75166 Antibody
3	65	69.9	59	6	ABU56843	Abu56843 BoNT/A Hc
4	65	69.9	125	8	ADR38646	Adr38646 Mouse hea
5	64	68.8	52	6	ABU56891	Abu56891 BoNT/A Hc
6	62.5	67.2	19	2	AAW45497	Aaw45497 Targeting
7	62.5	67.2	19	2	ADH67963	Adh67963 Compositi
8	62.5	67.2	19	3	AAB20595	Aab20595 Glycoprot
9	62.5	67.2	19	5	ABG30388	Abg30388 Glycoprot
10	62.5	67.2	19	7	ABU63160	Abu63160 Targeting
11	62.5	67.2	21	2	AAW45498	Aaw45498 Targeting
12	62.5	67.2	21	2	ADH67964	Adh67964 Compositi
13	62.5	67.2	21	3	AAB20596	Aab20596 Glycoprot
14	62.5	67.2	21	5	ABG30389	Abg30389 Glycoprot
15	62.5	67.2	21	7	ABU63161	Abu63161 Targeting
16	62.5	67.2	21	8	ADM10973	Adm10973 GPIIbIIIa
17	62.5	67.2	26	2	AAR15276	Aar15276 Anti-thro
18	62.5	67.2	27	2	AAR15273	Aar15273 Anti-thro
19	62.5	67.2	127	2	AAR06355	Aar06355 Peptide c
20	62.5	67.2	219	2	AAR56235	Aar56235 h66-118/h
21	62.5	67.2	223	2	AAR56236	Aar56236 l66-111/1
22	59	63.4	59	6	ABU56892	Abu56892 BoNT/A Hc
23	59	63.4	125	8	ADR38648	Adr38648 Mouse hea
24	56	60.2	20	2	AAR15291	Aar15291 MRU for p
25	56	60.2	120	2	AAR25204	Aar25204 OP-G2 mon
26	55	59.1	120	2	AAR34262	Aar34262 Mab32 V-g
27	55	59.1	120	4	AAG62950	Aag62950 Amino aci
28	55	59.1	121	4	AAU02574	Aau02574 Anti-adip
29	55	59.1	246	2	AAR60522	Aar60522 Anti-TNF
30	53.5	57.5	291	6	ABR42054	Abr42054 Newcastle
31	53	57.0	17	5	ABP52337	Abp52337 Fv region
32	53	57.0	17	5	ABP52329	Abp52329 Fv region
33	53	57.0	144	5	ABB79730	Abb79730 Anti-Stre
34	53	57.0	155	6	ABP72295	Abp72295 Chimeric
35	53	57.0	155	8	ADQ15508	Adq15508 Dhvar1-li
36	53	57.0	165	6	ABP72294	Abp72294 Chimeric
37	53	57.0	165	8	ADQ15506	Adq15506 Histatin
38	53	57.0	232	9	ADX18570	Adx18570 VEGF-spec
39	53	57.0	232	9	AEA14680	Aea14680 VEGF rela
40	53	57.0	232	9	AEA13850	Aea13850 VEGF rela
41	52.5	56.5	26	2	AAR15277	Aar15277 Anti-thro
42	52.5	56.5	27	2	AAR15274	Aar15274 Anti-thro
43	52	55.9	15	8	ADR45758	Adr45758 Peptide d
44	52	55.9	24	8	ADR45759	Adr45759 Peptide d
45	52	55.9	28	2	AAR15275	Aar15275 Anti-thro
46	52	55.9	29	8	ADR45766	Adr45766 Heavy cha
47	52	55.9	263	2	AAW90226	Aaw90226 Anti-B7.2
48	52	55.9	268	2	AAW90222	Aaw90222 Anti-B7.2
49	52	55.9	276	2	AAW90227	Aaw90227 Anti-B7.1
50	52	55.9	281	2	AAW90223	Aaw90223 Anti-B7.1
51	52	55.9	403	4	ABG24933	Abg24933 Novel hum
52	52	55.9	556	2	AAW90218	Aaw90218 Bispecifi
53	52	55.9	580	2	AAW90217	Aaw90217 Bispecifi
54	51.5	55.4	291	4	AAB20443	Aab20443 Antibody
55	51.5	55.4	322	4	AAB20440	Aab20440 Antibody
56	51.5	55.4	729	4	AAB20439	Aab20439 Antibody
57	50.5	54.3	269	4	AAB61541	Aab61541 3DX sFv p

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OM protein - protein search, using sw model

Run on: August 9, 2006, 08:17:00 ; Search time 10.5392 Seconds
(without alignments)
132.883 Million cell updates/sec

Title: US-10-661-366-8
Perfect score: 93
Sequence: 1 SAYYRYDGSYYYAMDY 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Issued_Patents_AA:*
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3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	62.5	67.2	19	2	US-08-993-165-12	Sequence 12, Appl
2	62.5	67.2	19	2	US-09-540-448-12	Sequence 12, Appl
3	62.5	67.2	19	2	US-09-243-640-10	Sequence 10, Appl

4	62.5	67.2	19	2	US-08-929-847-12	Sequence 12, Appl
5	62.5	67.2	19	2	US-09-813-484-12	Sequence 12, Appl
6	62.5	67.2	19	2	US-10-046-801-12	Sequence 12, Appl
7	62.5	67.2	21	2	US-08-993-165-13	Sequence 13, Appl
8	62.5	67.2	21	2	US-09-540-448-13	Sequence 13, Appl
9	62.5	67.2	21	2	US-09-243-640-11	Sequence 11, Appl
10	62.5	67.2	21	2	US-08-929-847-13	Sequence 13, Appl
11	62.5	67.2	21	2	US-09-813-484-13	Sequence 13, Appl
12	62.5	67.2	21	2	US-10-046-801-13	Sequence 13, Appl
13	62.5	67.2	26	7	5196510-15	Patent No. 5196510
14	62.5	67.2	27	7	5196510-12	Patent No. 5196510
15	56	60.2	20	1	US-08-127-351-21	Sequence 21, Appl
16	56	60.2	20	1	US-08-480-367B-21	Sequence 21, Appl
17	56	60.2	20	1	US-08-487-221A-21	Sequence 21, Appl
18	56	60.2	20	1	US-08-480-370-21	Sequence 21, Appl
19	56	60.2	20	7	5196510-29	Patent No. 5196510
20	56	60.2	20	7	5196510-30	Patent No. 5196510
21	56	60.2	27	7	5196510-25	Patent No. 5196510
22	55	59.1	113	1	US-08-211-202-115	Sequence 115, App
23	55	59.1	120	1	US-08-211-202-1	Sequence 1, Appli
24	55	59.1	246	1	US-08-469-486-57	Sequence 57, Appl
25	55	59.1	246	1	US-08-469-658-57	Sequence 57, Appl
26	54.5	58.6	27	7	5196510-1	Patent No. 5196510
27	52.5	56.5	21	1	US-07-965-674-15	Sequence 15, Appl
28	52.5	56.5	21	5	PCT-US93-09523-15	Sequence 15, Appl
29	52.5	56.5	26	7	5196510-16	Patent No. 5196510
30	52.5	56.5	27	7	5196510-13	Patent No. 5196510
31	52	55.9	28	7	5196510-14	Patent No. 5196510
32	51.5	55.4	291	3	US-09-661-992B-102	Sequence 102, App
33	51.5	55.4	322	3	US-09-661-992B-96	Sequence 96, Appl
34	51.5	55.4	729	3	US-09-661-992B-94	Sequence 94, Appl
35	50	53.8	158	2	US-10-226-795-32	Sequence 32, Appl
36	49.5	53.2	124	2	US-08-767-128-38	Sequence 38, Appl
37	49.5	53.2	125	1	US-08-561-521-44	Sequence 44, Appl
38	49.5	53.2	125	5	PCT-US95-01219-44	Sequence 44, Appl
39	49	52.7	137	2	US-08-444-644-17	Sequence 17, Appl
40	49	52.7	137	2	US-08-232-246A-17	Sequence 17, Appl
41	49	52.7	233	2	US-08-444-644-33	Sequence 33, Appl
42	49	52.7	233	2	US-08-232-246A-33	Sequence 33, Appl
43	49	52.7	235	2	US-08-444-644-19	Sequence 19, Appl
44	49	52.7	235	2	US-08-444-644-28	Sequence 28, Appl
45	49	52.7	235	2	US-08-444-644-42	Sequence 42, Appl
46	49	52.7	235	2	US-08-232-246A-19	Sequence 19, Appl
47	49	52.7	235	2	US-08-232-246A-28	Sequence 28, Appl
48	49	52.7	235	2	US-08-232-246A-42	Sequence 42, Appl
49	48.5	52.2	13	5	PCT-US93-08435-20	Sequence 20, Appl
50	48.5	52.2	118	5	PCT-US93-08435-10	Sequence 10, Appl
51	48.5	52.2	122	5	PCT-US93-08435-12	Sequence 12, Appl
52	48.5	52.2	122	5	PCT-US93-08435-14	Sequence 14, Appl
53	48.5	52.2	122	5	PCT-US93-08435-43	Sequence 43, Appl
54	48	51.6	14	2	US-10-226-795-35	Sequence 35, Appl
55	48	51.6	106	2	US-09-198-452A-1098	Sequence 1098, Ap
56	48	51.6	108	2	US-09-438-185A-1024	Sequence 1024, Ap
57	47.5	51.1	122	2	US-09-232-290-41	Sequence 41, Appl
58	47.5	51.1	139	1	US-08-253-877C-19	Sequence 19, Appl
59	47.5	51.1	139	1	US-08-452-164A-19	Sequence 19, Appl
60	47.5	51.1	139	2	US-08-603-024-18	Sequence 18, Appl
61	47.5	51.1	139	2	US-08-450-809-14	Sequence 14, Appl
62	47.5	51.1	249	2	US-09-297-181-4	Sequence 4, Appli
63	47	50.5	113	1	US-08-273-146-59	Sequence 59, Appl
64	47	50.5	525	2	US-09-113-750A-35	Sequence 35, Appl

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OM protein - protein search, using sw model

Run on: August 9, 2006, 09:01:05 ; Search time 34.2389 Seconds
(without alignments)
216.462 Million cell updates/sec

Title: US-10-661-366-8
Perfect score: 93
Sequence: 1 SAYYRYDGSYYYAMDY 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

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3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	93	100.0	125	5 US-10-661-366-1	Sequence 1, Appli
3	65	69.9	125	3 US-09-144-886-51	Sequence 51, Appli

4	65	69.9	125	4	US-10-632-706-48	Sequence 48, Appl
5	64	68.8	125	3	US-09-144-886-52	Sequence 52, Appl
6	62.5	67.2	19	3	US-09-813-484-12	Sequence 12, Appl
7	62.5	67.2	19	4	US-10-046-801-12	Sequence 12, Appl
8	62.5	67.2	21	3	US-09-813-484-13	Sequence 13, Appl
9	62.5	67.2	21	4	US-10-046-801-13	Sequence 13, Appl
10	59	63.4	125	3	US-09-144-886-53	Sequence 53, Appl
11	59	63.4	125	4	US-10-632-706-50	Sequence 50, Appl
12	53	57.0	17	4	US-10-470-045-63	Sequence 63, Appl
13	53	57.0	17	4	US-10-470-045-84	Sequence 84, Appl
14	53	57.0	125	3	US-09-910-358D-4	Sequence 4, Appli
15	53	57.0	125	3	US-09-910-358D-8	Sequence 8, Appli
16	53	57.0	144	3	US-09-881-823-12	Sequence 12, Appl
17	53	57.0	155	4	US-10-077-624-7	Sequence 7, Appli
18	53	57.0	155	4	US-10-706-391-4	Sequence 4, Appli
19	53	57.0	165	4	US-10-077-624-4	Sequence 4, Appli
20	53	57.0	165	4	US-10-706-391-2	Sequence 2, Appli
21	52	55.9	15	4	US-10-772-089-3	Sequence 3, Appli
22	52	55.9	24	4	US-10-772-089-4	Sequence 4, Appli
23	52	55.9	201	4	US-10-424-599-182840	Sequence 182840,
24	52	55.9	403	5	US-10-450-763-55292	Sequence 55292, A
25	51.5	55.4	291	6	US-11-093-103-102	Sequence 102, App
26	51.5	55.4	322	6	US-11-093-103-96	Sequence 96, Appl
27	51.5	55.4	729	6	US-11-093-103-94	Sequence 94, Appl
28	50.5	54.3	269	4	US-10-027-770-2	Sequence 2, Appli
29	50.5	54.3	269	4	US-10-027-770-5	Sequence 5, Appli
30	50.5	54.3	451	4	US-10-679-620-78	Sequence 78, Appl
31	50.5	54.3	451	6	US-11-132-143-78	Sequence 78, Appl
32	50.5	54.3	512	4	US-10-679-620-70	Sequence 70, Appl
33	50.5	54.3	512	6	US-11-132-143-70	Sequence 70, Appl
34	50.5	54.3	517	4	US-10-679-620-68	Sequence 68, Appl
35	50.5	54.3	517	6	US-11-132-143-68	Sequence 68, Appl
36	50.5	54.3	519	4	US-10-679-620-66	Sequence 66, Appl
37	50.5	54.3	519	6	US-11-132-143-66	Sequence 66, Appl
38	50.5	54.3	552	4	US-10-679-620-86	Sequence 86, Appl
39	50.5	54.3	552	6	US-11-132-143-86	Sequence 86, Appl
40	50.5	54.3	712	4	US-10-679-620-116	Sequence 116, App
41	50.5	54.3	712	6	US-11-132-143-116	Sequence 116, App
42	50.5	54.3	713	4	US-10-679-620-64	Sequence 64, Appl
43	50.5	54.3	713	6	US-11-132-143-64	Sequence 64, Appl
44	50.5	54.3	715	4	US-10-679-620-62	Sequence 62, Appl
45	50.5	54.3	715	6	US-11-132-143-62	Sequence 62, Appl
46	50	53.8	120	4	US-10-372-719-2	Sequence 2, Appli
47	50	53.8	120	5	US-10-505-747-2	Sequence 2, Appli
48	50	53.8	125	4	US-10-041-860-42	Sequence 42, Appl
49	50	53.8	125	4	US-10-041-860-207	Sequence 207, App
50	50	53.8	125	4	US-10-665-383-62	Sequence 62, Appl
51	50	53.8	158	4	US-10-226-795-32	Sequence 32, Appl
52	49.5	53.2	125	5	US-10-763-424-70	Sequence 70, Appl
53	49.5	53.2	125	5	US-10-763-539-70	Sequence 70, Appl
54	49.5	53.2	125	6	US-11-096-074-57	Sequence 57, Appl
55	49.5	53.2	125	6	US-11-095-822-57	Sequence 57, Appl
56	49.5	53.2	126	4	US-10-041-860-354	Sequence 354, App
57	49	52.7	254	6	US-11-017-030-1	Sequence 1, Appli
58	49	52.7	260	5	US-10-935-290-116	Sequence 116, App
59	49	52.7	471	6	US-11-031-485-38	Sequence 38, Appl
60	48	51.6	14	4	US-10-226-795-35	Sequence 35, Appl
61	48	51.6	15	5	US-10-903-858-21	Sequence 21, Appl
62	48	51.6	99	4	US-10-312-273-199	Sequence 199, App
63	48	51.6	106	4	US-10-289-762-1098	Sequence 1098, Ap
64	48	51.6	121	4	US-10-308-817-187	Sequence 187, App

SCORE Search Results Details for Application 10661366 and Search Result us-10-661-366-8.ra

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OM protein - protein search, using sw model

Run on: August 9, 2006, 09:02:15 ; Search time 5.24232 Seconds
(without alignments)
205.442 Million cell updates/sec

Title: US-10-661-366-8
Perfect score: 93
Sequence: 1 SAYYRYDGSYYYAMDY 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 239914 seqs, 67312017 residues

Total number of hits satisfying chosen parameters: 239914

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Published_Applications_AA_New:*
1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
8: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	51.5	55.4	119	6 US-10-968-757-17	Sequence 17, Appl

2	49.5	53.2	125	7	US-11-006-808-44	Sequence 44, Appl
3	47	50.5	228	7	US-11-056-355B-19360	Sequence 19360, A
4	47	50.5	270	7	US-11-056-355B-19359	Sequence 19359, A
5	47	50.5	277	7	US-11-056-355B-19358	Sequence 19358, A
6	46.5	50.0	120	7	US-11-375-221-104	Sequence 104, App
7	46	49.5	117	6	US-10-968-757-22	Sequence 22, Appl
8	46	49.5	371	6	US-10-449-902-47811	Sequence 47811, A
9	46	49.5	387	7	US-11-058-746-5	Sequence 5, Appli
10	45	48.4	119	7	US-11-304-986-25	Sequence 25, Appl
11	45	48.4	120	7	US-11-183-218-36	Sequence 36, Appl
12	45	48.4	120	7	US-11-256-060-6	Sequence 6, Appli
13	45	48.4	120	7	US-11-024-877-11	Sequence 11, Appl
14	45	48.4	120	7	US-11-304-986-21	Sequence 21, Appl
15	45	48.4	120	7	US-11-304-986-22	Sequence 22, Appl
16	45	48.4	120	7	US-11-304-986-24	Sequence 24, Appl
17	45	48.4	121	7	US-11-304-986-23	Sequence 23, Appl
18	45	48.4	123	7	US-11-304-986-27	Sequence 27, Appl
19	45	48.4	234	7	US-11-155-909-31	Sequence 31, Appl
20	45	48.4	252	7	US-11-024-877-1	Sequence 1, Appli
21	45	48.4	278	7	US-11-155-909-26	Sequence 26, Appl
22	45	48.4	280	7	US-11-155-909-28	Sequence 28, Appl
23	45	48.4	449	7	US-11-254-182-14	Sequence 14, Appl
24	45	48.4	449	7	US-11-295-229-14	Sequence 14, Appl
25	45	48.4	449	7	US-11-154-091-16	Sequence 16, Appl
26	45	48.4	461	7	US-11-199-062-26	Sequence 26, Appl
27	44.5	47.8	249	7	US-11-330-353-18	Sequence 18, Appl
28	44	47.3	120	7	US-11-290-687-70	Sequence 70, Appl
29	44	47.3	120	7	US-11-304-986-26	Sequence 26, Appl
30	44	47.3	239	6	US-10-471-571A-4876	Sequence 4876, Ap
31	43	46.2	17	6	US-10-539-402-84	Sequence 84, Appl
32	43	46.2	248	6	US-10-539-402-14	Sequence 14, Appl
33	43	46.2	438	6	US-10-953-349-8788	Sequence 8788, Ap
34	43	46.2	438	7	US-11-056-355B-23717	Sequence 23717, A
35	43	46.2	438	7	US-11-056-355B-34714	Sequence 34714, A
36	43	46.2	438	7	US-11-056-355B-46355	Sequence 46355, A
37	43	46.2	438	7	US-11-056-355B-79204	Sequence 79204, A
38	43	46.2	537	6	US-10-953-349-8787	Sequence 8787, Ap
39	43	46.2	537	7	US-11-056-355B-23716	Sequence 23716, A
40	43	46.2	537	7	US-11-056-355B-34713	Sequence 34713, A
41	43	46.2	537	7	US-11-056-355B-46354	Sequence 46354, A
42	43	46.2	537	7	US-11-056-355B-79203	Sequence 79203, A
43	43	46.2	541	6	US-10-953-349-8786	Sequence 8786, Ap
44	43	46.2	541	7	US-11-056-355B-23715	Sequence 23715, A
45	43	46.2	541	7	US-11-056-355B-34712	Sequence 34712, A
46	43	46.2	541	7	US-11-056-355B-46353	Sequence 46353, A
47	43	46.2	541	7	US-11-056-355B-79202	Sequence 79202, A
48	42	45.2	568	7	US-11-056-355B-17654	Sequence 17654, A
49	42	45.2	597	7	US-11-056-355B-17653	Sequence 17653, A
50	42	45.2	635	7	US-11-056-355B-17652	Sequence 17652, A
51	41.5	44.6	124	6	US-10-541-708-29	Sequence 29, Appl
52	41.5	44.6	139	7	US-11-224-664-37	Sequence 37, Appl
53	41	44.1	258	6	US-10-449-902-47896	Sequence 47896, A
54	41	44.1	485	7	US-11-174-307B-3070	Sequence 3070, Ap
55	40	43.0	120	6	US-10-529-835-1	Sequence 1, Appli
56	40	43.0	120	7	US-11-290-687-61	Sequence 61, Appl
57	40	43.0	120	7	US-11-290-687-72	Sequence 72, Appl
58	40	43.0	120	7	US-11-301-373-2	Sequence 2, Appli
59	40	43.0	120	7	US-11-301-373-45	Sequence 45, Appl
60	40	43.0	121	6	US-10-499-266-2	Sequence 2, Appli
61	40	43.0	204	7	US-11-056-355B-28877	Sequence 28877, A
62	40	43.0	204	7	US-11-056-355B-32467	Sequence 32467, A

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OM protein - protein search, using sw model

Run on: August 9, 2006, 08:00:49 ; Search time 6.27986 Seconds
 (without alignments)
 245.144 Million cell updates/sec

Title: US-10-661-366-8
 Perfect score: 93
 Sequence: 1 SAYYRYDGSYYYAMDY 16

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 1000 summaries

Database : PIR_80:*
 1: pir1:*
 2: pir2:*
 3: pir3:*
 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%					Description
	Query	Match	Length	DB	ID	
No.	Score					
1	73	78.5	119	2	E25114	Ig heavy chain V r
2	63	67.7	119	2	D25114	Ig heavy chain V r
3	63	67.7	119	2	A43413	Ig heavy chain V r
4	62.5	67.2	127	2	B31807	Ig heavy chain V r
5	60.5	65.1	19	2	PH1609	Ig H chain V-D-J r
6	60	64.5	17	2	PH1607	Ig H chain V-D-J r
7	52	55.9	123	2	G48677	Ig heavy chain V-D
8	52	55.9	123	2	F48677	Ig heavy chain V-D

9	52	55.9	123	2	E48677	Ig heavy chain V-D
10	52	55.9	900	2	E69631	galactosamine-cont
11	51	54.8	16	2	PH1589	Ig H chain V-D-J r
12	50.5	54.3	131	2	S66537	Ig heavy chain V r
13	50	53.8	14	2	PH1608	Ig H chain V-D-J r
14	50	53.8	119	2	C25114	Ig heavy chain V r
15	49.5	53.2	109	2	S26318	Ig heavy chain V r
16	49	52.7	99	2	S26326	Ig heavy chain V r
17	49	52.7	106	2	S14489	Ig heavy chain V r
18	49	52.7	109	2	PH1023	Ig heavy chain V r
19	49	52.7	121	2	S55540	Ig heavy chain V r
20	48	51.6	99	2	D86618	hypothetical prote
21	48	51.6	99	2	A72005	hypothetical prote
22	48	51.6	115	2	PC6026	acetylcholine recep
23	48	51.6	233	2	C86849	regulatory protein
24	47.5	51.1	15	2	PH1610	Ig H chain V-D-J r
25	47.5	51.1	119	2	C53285	Ig heavy chain V a
26	47.5	51.1	129	2	S46393	Ig heavy chain V r
27	47	50.5	109	2	S26325	Ig heavy chain V r
28	47	50.5	264	2	H69800	hypothetical prote
29	46	49.5	16	2	PH1588	Ig H chain V-D-J r
30	46	49.5	178	2	S29594	Ig gamma chain (WM
31	46	49.5	239	2	G89867	hypothetical prote
32	46	49.5	387	2	T09839	oleate 12-hydroxyl
33	46	49.5	511	2	S24345	Balbani ring 1 pr
34	46	49.5	955	2	A60990	alpha-amylase (EC
35	46	49.5	958	2	E83701	alpha-amylase G-6
36	46	49.5	1599	2	S22737	glucosyltransferas
37	45	48.4	12	2	PH1606	Ig H chain V-D-J r
38	45	48.4	14	2	PH1597	Ig H chain V-D-J r
39	45	48.4	117	2	S38563	Ig heavy chain V r
40	45	48.4	118	2	A49026	Ig heavy chain V r
41	45	48.4	118	2	E27889	Ig heavy chain V r
42	45	48.4	119	2	PH0099	Ig heavy chain V r
43	45	48.4	119	2	PL0085	Ig heavy chain V r
44	45	48.4	139	2	A27609	Ig heavy chain pre
45	45	48.4	786	2	A69927	ribonucleoside-dip
46	45	48.4	1084	2	T12925	ribunucleotide red
47	44.5	47.8	102	2	S14581	Ig heavy chain V r
48	44.5	47.8	111	2	PH0993	Ig heavy chain V r
49	44	47.3	121	2	D30560	Ig heavy chain V r
50	44	47.3	122	2	S20809	Ig heavy chain V r
51	44	47.3	513	2	H69735	endo-1,4-beta-xyla
52	43.5	46.8	139	2	A32456	Ig heavy chain pre
53	43	46.2	13	2	PH1596	Ig H chain V-D-J r
54	43	46.2	14	2	PH1601	Ig H chain V-D-J r
55	43	46.2	94	2	PH0996	Ig heavy chain V r
56	43	46.2	121	2	B34871	Ig heavy chain V r
57	43	46.2	194	2	F86689	prophage ps2 prote
58	43	46.2	285	2	C64750	probable transcrip
59	43	46.2	477	2	A97176	glycogen synthase,
60	43	46.2	541	2	S56653	thioglucohydrolase (E
61	43	46.2	631	2	AD2224	hypothetical prote
62	43	46.2	635	2	S19011	endo-1,4-beta-xyla
63	42.5	45.7	375	2	S49767	heat shock protein
64	42	45.2	95	2	G37262	Ig heavy chain V r
65	42	45.2	120	2	A25114	Ig heavy chain V r
66	42	45.2	127	2	S38489	Ig heavy chain - h
67	42	45.2	128	2	S48797	Ig heavy chain V r
68	42	45.2	300	2	AE1380	internalin homolog
69	42	45.2	312	2	F72291	hypothetical prote

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OM protein - protein search, using sw model

Run on: August 9, 2006, 07:46:18 ; Search time 48.3823 Seconds
(without alignments)
305.902 Million cell updates/sec

Title: US-10-661-366-8
Perfect score: 93
Sequence: 1 SAYYRYDGSYYYAMDY 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	73	78.5	119	2	Q53VQ5_MOUSE
2	63	67.7	119	2	Q53VQ9_MOUSE
3	62	66.7	145	2	Q924R1_MOUSE
4	58	62.4	483	2	Q5U413_MOUSE

5	53	57.0	145	2	Q924P7_MOUSE	Q924p7	mus musculu
6	52	55.9	900	1	GGAB_BACSU	P46918	bacillus su
7	51	54.8	193	2	Q4JLH3_LACRE	Q4jhlh3	lactobacill
8	51	54.8	214	2	Q7VL60_HAEDU	Q7vl60	haemophilus
9	51	54.8	485	2	Q561M5_MOUSE	Q561m5	mus musculu
10	50	53.8	119	2	Q53VR3_MOUSE	Q53vr3	mus musculu
11	50	53.8	155	2	Q8FNU6_COREF	Q8fnu6	corynebacte
12	49	52.7	110	2	Q4ZC53_9CAUD	Q4zc53	bacterioph
13	49	52.7	379	2	Q6FVM1_CANGA	Q6fvm1	candida gla
14	49	52.7	449	2	Q86GG0_PENJP	Q86gg0	penaeus jap
15	49	52.7	791	2	Q37WQ7_SPHAR	Q37wq7	novosphingo
16	48	51.6	99	2	Q9Z6N6_CHLPN	Q9z6n6	chlamydia p
17	48	51.6	233	1	MECA_LACLA	Q9cep1	lactococcus
18	48	51.6	273	2	Q9M4Z0_9LILI	Q9m4z0	dioscorea a
19	48	51.6	330	2	Q2ND18_9SPHN	Q2nd18	erythrobact
20	48	51.6	1184	2	Q4QBX8_LEIMA	Q4qbx8	leishmania
21	48	51.6	1604	2	Q5CW61_CRYPV	Q5cw61	cryptospori
22	47	50.5	264	1	RECX_BACSU	O31575	bacillus su
23	47	50.5	291	2	Q75KB4_ORYSA	Q75kb4	oryza sativ
24	47	50.5	351	2	Q514R4_ENTHI	Q514r4	entamoeba h
25	47	50.5	362	2	Q4WQC9_ASFFU	Q4wqc9	aspergillus
26	47	50.5	391	2	Q64ZE4_BACFR	Q64ze4	bacteroides
27	47	50.5	403	2	Q5LIC4_BACFN	Q5lic4	bacteroides
28	47	50.5	484	2	Q3KQK0_MOUSE	Q3kqk0	mus musculu
29	47	50.5	654	2	Q61YG3_CAEER	Q61yg3	caenorhabdi
30	47	50.5	712	2	Q750I9_ASHGO	Q750i9	ashbya goss
31	47	50.5	714	2	Q4CW30_TRYCR	Q4cw30	trypanosoma
32	47	50.5	714	2	Q4D6H1_TRYCR	Q4d6h1	trypanosoma
33	47	50.5	714	2	Q94795_TRYCR	Q94795	trypanosoma
34	47	50.5	714	2	Q41CA6_9BACI	Q41ca6	exiguobacte
35	46.5	50.0	624	2	Q6NS22_XENLA	Q6ns22	xenopus lae
36	46.5	50.0	711	2	Q6CIR5_KLULA	Q6cir5	kluyveromyc
37	46	49.5	95	2	Q822E5_CHLCV	Q822e5	chlamydophi
38	46	49.5	96	2	Q67UA6_ORYSA	Q67ua6	oryza sativ
39	46	49.5	113	2	Q3P2M1_9GAMM	Q3p2m1	shewanella
40	46	49.5	152	2	Q4BMS4_BURVI	Q4bms4	burkholderi
41	46	49.5	153	2	Q3CLB3_ALTAT	Q3clb3	pseudoalter
42	46	49.5	239	1	MECA_STAAM	P60184	staphylococ
43	46	49.5	239	1	MECA_STAAN	P60185	staphylococ
44	46	49.5	239	1	MECA_STAAR	Q6gi87	staphylococ
45	46	49.5	239	1	MECA_STAAS	Q6gas8	staphylococ
46	46	49.5	239	1	MECA_STAAB	P60186	staphylococ
47	46	49.5	239	2	Q2YWY4_STAAB	Q2ywy4	staphylococ
48	46	49.5	331	2	Q5L1Q3_GEOKA	Q5l1q3	geobacillus
49	46	49.5	347	1	CLH0_CHEAL	Q91e89	chenopodium
50	46	49.5	371	2	Q94D47_ORYSA	Q94d47	oryza sativ
51	46	49.5	387	2	Q41131_RICCO	Q41131	ricinus com
52	46	49.5	511	2	Q00625_CHITE	Q00625	chironomus
53	46	49.5	598	2	Q568Y0_RAT	Q568y0	rattus norv
54	46	49.5	703	2	Q3P673_9GAMM	Q3p673	shewanella
55	46	49.5	955	2	Q45574_BACSP	Q45574	bacillus sp
56	46	49.5	955	2	Q5WHK9_BACSK	Q5whk9	bacillus cl
57	46	49.5	958	2	Q5GIA5_BACHD	Q5gia5	bacillus ha
58	46	49.5	958	2	Q9KFR4_BACHD	Q9kfr4	bacillus ha
59	46	49.5	1599	2	Q00599_STRSL	Q00599	streptococc
60	46	49.5	1989	2	Q4BXB6_CROWT	Q4bxb6	crocospaer
61	45	48.4	48	1	CU6B_LIMPO	P83358	limulus pol
62	45	48.4	315	2	Q3CKX6_ALTAT	Q3ckx6	pseudoalter
63	45	48.4	396	1	PRIL_PYRFU	Q8u4h7	pyrococcus
64	45	48.4	402	2	Q8I2E1_PLAF7	Q8i2e1	plasmodium
65	45	48.4	486	2	Q4AFM9_9CHLB	Q4afm9	chlorobium